

CTG GYN GCT GGT TAT GCT CAT GAT GAT GAC TGG ATT GAC CCC ACA GAC	219
Leu Xaa Ala Gly Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp	
-5 1 5 10	
ATG CTT AAC TAT GAT GCT GCT TCA GGA ACA ATG AGA AAA TCT CAG GCA	267
Met Leu Asn Tyr Asp Ala Ala Ser Gly Thr Met Arg Lys Ser Gln Ala	
15 20 25	
AAA TAT GGT ATT TCA GGG GAA AAG GAT GTC AGT CCT GAC TTG TCA TGT	315
Lys Tyr Gly Ile Ser Gly Glu Lys Asp Val Ser Pro Asp Leu Ser Cys	
30 35 40	
GCT GRT GAA ATA TCA GAA	333
Ala Xaa Glu Ile Ser Glu	
45	

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 129..278
id R18809
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 71..129
id R18809
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 323..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 299..347
id R18809
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..441
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 141..277
id R88070
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..300
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..134
id R88070
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..307
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 68..217
id T85919
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 98..157
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 9..68
id T85919
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..317
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 129..288
id R60434
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 99..157
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 71..129
id R60434
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..307
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 86..235
id W23910
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 27..86
id W23910
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 325..381
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq LVXSLPVHCLTFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

AAGTTGGTGG AGTTCTGCCC GGATGGAAGC TCCGGCCGCG GAGTGATGGT GGCCTCAGCG      60
AAGATGGGCC GGGCAGGGAC CATGGCGGTG GCAGCAGAGC TTCGAGAGCT GTGCCCAGGA    120
GTGAACAACC AGCCCTACCT CTGTGAGAGT KGTCACCTGC TCGGGGAAM CTGGCTGCTG    180
CACCTACTAC TATGAGCTCT GGTGGTTCTG GCTGCTCTGG ACTGTCCTCA TCCTCTTTAG    240
CTGCTGTTGC GCCTCCGCC ACCGACGAGC TAAACTCAGG CTGCAACAAC AGCAGCGGCA    300
SSTGAAACAA CTTGTTGGCC TATC ATG GGG CAT GCC ATG GGG CTG GTN STT      351
                Met Gly His Ala Met Gly Leu Val Xaa
                -15

TCC CTA CCG GTT CAC TGC TTG ACC TTC GCT TCC TCA GCA CCT TCA AGC      399
Ser Leu Pro Val His Cys Leu Thr Phe Ala Ser Ser Ala Pro Ser Ser
-10                -5                1                5

CCC CAG CCT ACG AGG ATG TGG TTC AMC GCC CAG GCA CAC CAM CCC CCC      447
Pro Gln Pro Thr Arg Met Trp Phe Xaa Ala Gln Ala His Xaa Pro Pro
                10                15                20

CTT ATA CTG GGC CCG                                          462
Leu Ile Leu Gly Pro
                25

```

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 156..288
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..133
id AA081350
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 289..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 133..240
id AA081350
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 422..453
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 269..300
id AA081350
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 289..453
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 67..231
id AA046671
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..289
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..68
id AA046671
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 104..151
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWTR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AATAGTTCCA GAACTCTCCA TCCGGACTAG TTATTGAGCA TCTGCCTCTC ATATCACCAG 60

TGGCCATCTG AGGTGTTTCC CTGGCTCTGA AGGGGTAGGC ACG ATG GCC AGG TGC 115
Met Ala Arg Cys

-15

TTC AGC CTG GTG TTG CTT CTC ACT TCC ATC TGG ACC ACG AGG CTC CTG	163
Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr Thr Arg Leu Leu	
-10 -5 1	
GTC CAA GGC TCT TTG CGT GCA GAA GAG CTT TCC ATC CAG GTG TCA TGC	211
Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile Gln Val Ser Cys	
5 10 15 20	
AGA ATT ATG GGG ATC ACC CTT GTG AGC AAA AAG GCG AAC CAG CAG CTG	259
Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala Asn Gln Gln Leu	
25 30 35	
AAT TTC ACA GAA GCT AAG GAG GCC TGT AGG CTG CTG GGA CTA AGT TTG	307
Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu Gly Leu Ser Leu	
40 45 50	
GCC GGC AAG GAC CAA GTT GAA ACA GCC TTG AAA GCT AGC TTT GAA ACT	355
Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala Ser Phe Glu Thr	
55 60 65	
TGC AGC TAT GGC TGG GTT GGA GAT GGA TTC GTG GTC ATC TCT AGG ATT	403
Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val Ile Ser Arg Ile	
70 75 80	
AGC CCA AAC CCC AAG TGT GGG AAA AAT GGG GTG GGT GTC CTG ATT TGG	451
Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly Val Leu Ile Trp	
85 90 95 100	

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 67..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..301
id AA056199
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 152..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..215

id R66275
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..221
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 99..203
id AA054476
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..120
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 22..103
id AA054476
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 232..366
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..135
id AA143025
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 242..366
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 84..208
id W90481
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 175..351
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq VLAQLAFLSQISQ/CI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```
ACTTTTCCGG CTGACTTCTG AGAAGGTTGC GCASAGCTGT GCCCGGCAGT CTAGAGGCGC   60
AGAAGAGGAA GCCATCGCCT GGCCCCGGCT CTCTGGACCT TGTCTCGCTC GGGAGCGGAA  120
ACAGCGGCAG CCAGAGAACT GTTTTAATCA TGGACAAACA AAACTCACAG ATGA ATG      177
                                         Met
CTT CTC ACC CGG AAA CAA ACT TGC CAG TTG GGT ATC CTC CTC AGT ATC      225
Leu Leu Thr Arg Lys Gln Thr Cys Gln Leu Gly Ile Leu Leu Ser Ile
      -55                      -50                      -45
CAC CCA CAG CAT TCC AAG GAC CTC CAG GAT ATA GTG GCT ACC CTG GGC      273
```

His	Arg	Gln	His	Ser	Lys	Asp	Leu	Gln	Asp	Ile	Val	Ala	Thr	Leu	Gly	
		-40					-35					-30				
CCC	AGG	TCA	GCT	ACC	CAC	CCC	CAC	CAG	CCG	GCC	ATT	CAG	GTC	CTG	GCC	321
Pro	Arg	Ser	Ala	Thr	His	Pro	His	Gln	Pro	Ala	Ile	Gln	Val	Leu	Ala	
	-25					-20					-15					
CAG	CTG	GCT	TTC	CTG	TCC	CAA	ATC	AGC	CAG	TGT	ATA	ATC	AGC	CAG	CGG	369
Gln	Leu	Ala	Phe	Leu	Ser	Gln	Ile	Ser	Gln	Cys	Ile	Ile	Ser	Gln	Arg	
-10					-5					1				5		

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 166..300
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 92..226
id AA284366
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: 199..282
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
 seq IVSLLGFVATVTLL/IP
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

AGAACATAGG TTGCCTTAGA GAGGTTCCCC GGTGTCCCGA CGGCGGCTCA AGTCAGAGTT 60
GCTGGGTTTT GCTCAGATTG GTGTGGGAAG AGCCTGCCTG TGGGGAGCGG CCACTCCATA 120
CTGCTGARGC CTCAGGACTG CTGCTCAGCT TGCCCGTTAC CTGAAGAGGC GGCGGAGCGG 180
NGCCCCTGAC CGGTCACC ATG TGG GCC TTC TCG GAA TTG CCC ATG CCG CTG 231
 Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu
 -25 -20

CTG ATC AAT TTG ATC GTC TCG CTG CTG GGA TTT GTG GCC ACA GTC ACC 279
Leu Ile Asn Leu Ile Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr
 -15 -10 -5

CTC ATC CCG GCC TTC CGG GGC CAC TTC ATT GCT GCG CGC CTC TGT GGT 327
Leu Ile Pro Ala Phe Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly
 1 5 10 15

CAG GAC CTC AAC AAA ACC AGC CGA CAG CAG ATC CCA GAA TCC CAG GGA 375
Gln Asp Leu Asn Lys Thr Ser Arg Gln Gln Ile Pro Glu Ser Gln Gly
 20 25 30

GTG ATC AGC GGT GCT GTT TTC CTT ATC ATC CTC TTC TGC
Val Ile Ser Gly Ala Val Phe Leu Ile Ile Leu Phe Cys 414
 35 40

```

(2) INFORMATION FOR SEQ ID NO: 103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 241..373  
id H87867  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 63..159  
id H87867

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 201..240  
id H87867  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 224..459
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..236  
id N87591  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..453
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 65..255  
id AA172091  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 202..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 4..53  
id AA172091  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..459
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 38..234  
id H85080  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 225..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..37  
id H85080  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 212..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4

seq PASLSLLTFKVYA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

GACGCGCTGC GGCTCAGCGA CGCGGCTTCT AGAACCGGGT GATTGAACTA AACCTTCGCC 60
GCACCGAGTT TGCAGTACGG CCGTCACCCG CACCGCTGCC TGCTTGCGGT TGGAGAAATC 120
AARGGGCCCT ACCGGGCCTC CGTAGTCACC TCTCTATAGT GGGCGTGGCC GAGGCCGGGG 180
TGACCCTGCC GGAGCCTCCG CTGCCAGCGA C ATG TTC AAG GTA ATT CAG AGG 232
 Met Phe Lys Val Ile Gln Arg
 -20

TCC GTG GGG CCA GCC AGC CTG AGC TTG CTC ACC TTC AAA GTC TAT GCA 280
Ser Val Gly Pro Ala Ser Leu Ser Leu Leu Thr Phe Lys Val Tyr Ala
-15 -10 -5

GCA CCA AAA AAG GAC TCA CCT CCC AAA AAT TCC GTG AAG GTT GAT GAG 328
Ala Pro Lys Lys Asp Ser Pro Pro Lys Asn Ser Val Lys Val Asp Glu
 1 5 10 15

CTT TCA CTC TAC TCA GTT CCT GAG GGT CAA TCG AAG TAT GTG GAG GAG 376
Leu Ser Leu Tyr Ser Val Pro Glu Gly Gln Ser Lys Tyr Val Glu Glu
 20 25 30

GCA AGG AGC CAG CTT GAA GAA AGC ATC TCA CAG CTC CGA CAC TAT TGC 424
Ala Arg Ser Gln Leu Glu Glu Ser Ile Ser Gln Leu Arg His Tyr Cys
 35 40 45

GAG CCA TAC ACA ACC TGG TGT CAG GAA ACG TAC 457
Glu Pro Tyr Thr Thr Trp Cys Gln Glu Thr Tyr
 50 55

```

(2) INFORMATION FOR SEQ ID NO: 104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 38..251  
id T94226  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 225..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..149  
id W95280  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 371..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 148..214  
id W95280  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 2..124  
id N55978  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 262..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 98..162  
id N55978  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 379..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 270..328  
id N55978  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 317..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 154..210  
id N55978  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 20..427
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq LISVALVQGWALG/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

AACCGTGGCC TCGGACGAA ATG GCG AAA AGT CTT TTG AAG ACA GCC TCT CTG 52
 Met Ala Lys Ser Leu Leu Lys Thr Ala Ser Leu
 -135 -130

TCT GGA AGG ACA AAA TTG CTA CAT CAA ACA GGA TTG TCA CTT TAT AGT 100
Ser Gly Arg Thr Lys Leu Leu His Gln Thr Gly Leu Ser Leu Tyr Ser
-125 -120 -115 -110

ACA TCC CAT GGA TTT TAT GAG GAA GAA GTG AAA AAA ACA CTT CAG CAG 148
Thr Ser His Gly Phe Tyr Glu Glu Glu Val Lys Lys Thr Leu Gln Gln
 -105 -100 -95

TTT CCT GGT GGA TCC ATT GAC CTT CAG AAG GAA GAC AAT GGC ATT GGC 196
Phe Pro Gly Gly Ser Ile Asp Leu Gln Lys Glu Asp Asn Gly Ile Gly
 -90 -85 -80

ATT CTT ACT CTG AAC AAT CCA AGT AGA ATG AAT GCC TTT TCA GGT GTT 244
Ile Leu Thr Leu Asn Asn Pro Ser Arg Met Asn Ala Phe Ser Gly Val
 -75 -70 -65

ATG ATG CTA CAA CTT CTG GAA AAA GTA ATT GAA TTG GAA AAT TGG ACA 292
Met Met Leu Gln Leu Leu Glu Lys Val Ile Glu Leu Glu Asn Trp Thr
 -60 -55 -50

GAG GGG AAA GGC CTC ATT GTC CGT GGG GCA AAA AAT ACT TTC TCT TCA 340
Glu Gly Lys Gly Leu Ile Val Arg Gly Ala Lys Asn Thr Phe Ser Ser
-45 -40 -35 -30

GGA TCT GAT CTG AAT GCT GTG AAA TCA CTA GGA CTC CAG AGA CTT CCT 388
Gly Ser Asp Leu Asn Ala Val Lys Ser Leu Gly Leu Gln Arg Leu Pro
 -25 -20 -15

TTA ATA AGT GTT GCG CTG GTT CAA GGT TGG GCA TTG GGT GGA GGA GCA 436
Leu Ile Ser Val Ala Leu Val Gln Gly Trp Ala Leu Gly Gly Gly Ala
 -10 -5 1

GCG
Ala
839

```

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..212



(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 125..221  
 id HUMEST2D1  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 214..322  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 9..117  
 id AA115085  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 132..263  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.3  
 seq PLLKILHAAGAQG/EM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

AATTTCAVVA TGCTGCCGAG GCCCTAGGAT CTGTGACTGC CACCCCTCCC CCCACCCGGG 60
CTCGGCGGGG GAGCGACTCA TGGAGCTGCC GTAAGTTTTA CCAACAGACT GCAGTTTCTT 120
TCACTACCAA A ATG ACA TCA TTT TCC ACC TCT GCT CAG TGT TCA ACA TCT 170
 Met Thr Ser Phe Ser Thr Ser Ala Gln Cys Ser Thr Ser
 -40 -35

GAC AGT GCT TGC AGG ATC TCT CCT GGA CAA ATC AAT SVG GTA CGA CCA 218
Asp Ser Ala Cys Arg Ile Ser Pro Gly Gln Ile Asn Xaa Val Arg Pro
 -30 -25 -20

AAA CTG CCG CTT TTG AAG ATT TTG CAT GCA GCA GGT GCG CAA GGT GAA 266
Lys Leu Pro Leu Leu Lys Ile Leu His Ala Ala Gly Ala Gln Gly Glu
 -15 -10 -5 1

ATG TTC ACT GTT AAA GAG GTC ATG CAC TAT TTA GGT CAG TAC ATA ATG 314
Met Phe Thr Val Lys Glu Val Met His Tyr Leu Gly Gln Tyr Ile Met
 5 10 15

GTG AAG CAG 323
Val Lys Gln
 20

```

## (2) INFORMATION FOR SEQ ID NO: 106:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 104..370  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..267  
id AA114062  
est

## (ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 409..451  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 309..351  
id AA114062  
est

## (ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 388..420  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 287..319  
id AA114062  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 5..340  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq AFAWLGVVPLTAC/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AAAG ATG GAC ACC GCG GAG GAA GAC ATA TGT AGA GTG TGT CGG TCA GAA | 49  |
| Met Asp Thr Ala Glu Glu Asp Ile Cys Arg Val Cys Arg Ser Glu      |     |
| -110 -105 -100                                                   |     |
| GGA ACA CCT GAG AAA CCG CTT TAT CAT CCT TGT GTA TGT ACT GGC AGT  | 97  |
| Gly Thr Pro Glu Lys Pro Leu Tyr His Pro Cys Val Cys Thr Gly Ser  |     |
| -95 -90 -85                                                      |     |
| ATT AAG TTN GTC CAT CAA GAA TGC TTA GTT CAA TGG CTG AAA CAC AGT  | 145 |
| Ile Lys Xaa Val His Gln Glu Cys Leu Val Gln Trp Leu Lys His Ser  |     |
| -80 -75 -70                                                      |     |
| CGA AAA GAA TAC TGT GAA TTA TGC AAG CAC AGA TTT GCT TTT ACA CCA  | 193 |
| Arg Lys Glu Tyr Cys Glu Leu Cys Lys His Arg Phe Ala Phe Thr Pro  |     |
| -65 -60 -55 -50                                                  |     |
| ATT TAT TCT CCA GAT ATG CCT TCA CGG CTT CCA ATT CAA GAC ATA TTT  | 241 |
| Ile Tyr Ser Pro Asp Met Pro Ser Arg Leu Pro Ile Gln Asp Ile Phe  |     |
| -45 -40 -35                                                      |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GCT GGA CTG GTT ACA AGT ATT GGC ACT GCA ATA CGA TAT TGG TTT CAT | 289 |
| Ala Gly Leu Val Thr Ser Ile Gly Thr Ala Ile Arg Tyr Trp Phe His |     |
| -30 -25 -20                                                     |     |
| TAT ACA CTT GTG GCC TTT GCA TGG TTG GGA GTT GTT CCT CTT ACA GCA | 337 |
| Tyr Thr Leu Val Ala Phe Ala Trp Leu Gly Val Val Pro Leu Thr Ala |     |
| -15 -10 -5                                                      |     |
| TGC CGC ATC TAC AAG TGC TTG TTT ACT GGC TCC GTG AGC TCA CTA CTG | 385 |
| Cys Arg Ile Tyr Lys Cys Leu Phe Thr Gly Ser Val Ser Ser Leu Leu |     |
| 1 5 10 15                                                       |     |
| ACG CTG CCA TTA GAT ATG CTG TCA ACG GAA AAT TTG TTG GCA GAT TGT | 433 |
| Thr Leu Pro Leu Asp Met Leu Ser Thr Glu Asn Leu Leu Ala Asp Cys |     |
| 20 25 30                                                        |     |
| TTG CAG GGT TGT TTT GTG GTG ACG TGC ACA CTG TGT GCA TTC ATC     | 478 |
| Leu Gln Gly Cys Phe Val Val Thr Cys Thr Leu Cys Ala Phe Ile     |     |
| 35 40 45                                                        |     |

## (2) INFORMATION FOR SEQ ID NO: 107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 87..227  
id W31692  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..121
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..77  
id W31692  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 76..226  
id H46855

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..76  
id H46855  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 85..225  
id H49687  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..121
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..75  
id H49687  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 84..224  
id H50194  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..121
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..75  
id H50194  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 82..222  
id AA285085  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..73  
id AA285085  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 153..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq MLIMLGIFNVHS/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```
CCCTGCGAGG GCATCCTGGG CTTTCTCCCA CCGCTTTCCG AGCCCGCTTG CACCTCGGCG 60
ATCCCCGACT CCCTTCTTTA TGGCGTCGCT CCGTGTCTGT GGGCCGAAGC TGGCCGCCTG 120
CGGCATCGTG YRTCAGCGCC TGGGGAGTGA TC ATG TTG ATA ATG CTC GGA ATA 173
 Met Leu Ile Met Leu Gly Ile
 -10
TTT TTC AAT GTC CAT TCC GCT GTG TTG ATT GAG GAC GTT CCC TTC ACG 221
Phe Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr
 -5 1 5 10
GAG AAA GAT TTT GAG ANT GGC CCC CAG AAC ATA TAC AAC CTT TAC GAG 269
Glu Lys Asp Phe Glu Xaa Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu
 15 20 25
CAT GGG 275
His Gly
```

## (2) INFORMATION FOR SEQ ID NO: 108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 82..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..142  
id W24852  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 231..320

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
 region 150..239  
 id W24852  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 256..321  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 1..66  
 id AA129007  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 321..350  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 65..94  
 id AA129007  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 9..344  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.5  
 seq AAVAVGMLXASYA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AGAGGGTT ATG GGA GGG CTC TGG CGT CCT GGA TGG AGG TGC GTT CCT TTC | 50  |
| Met Gly Gly Leu Trp Arg Pro Gly Trp Arg Cys Val Pro Phe          |     |
| -110 -105 -100                                                   |     |
| TGT GGC TGG CGC TGG ATC CAC CCT GGG TCT CCA ACC AGG GCT GCA GAG  | 98  |
| Cys Gly Trp Arg Trp Ile His Pro Gly Ser Pro Thr Arg Ala Ala Glu  |     |
| -95 -90 -85                                                      |     |
| AGG GTA GAG CCG TTT CTT AGG CCA GAG TGG AGT GGG ACA GGA GGT GCC  | 146 |
| Arg Val Glu Pro Phe Leu Arg Pro Glu Trp Ser Gly Thr Gly Gly Ala  |     |
| -80 -75 -70                                                      |     |
| GAG AGA GGA CTG AGG TGG CTT GGG ACA TGG AAG CGC TGC AGC CTT CGA  | 194 |
| Glu Arg Gly Leu Arg Trp Leu Gly Thr Trp Lys Arg Cys Ser Leu Arg  |     |
| -65 -60 -55                                                      |     |
| GCC CGG CAT CCA GCA TTG CAG CCG CCG CGG CGG CCT AAG AGC TCG AAC  | 242 |
| Ala Arg His Pro Ala Leu Gln Pro Pro Arg Arg Pro Lys Ser Ser Asn  |     |
| -50 -45 -40 -35                                                  |     |
| CCT TTC ACA CGC GCG SKV GAG GAG GAR CGG CGG CGG MAG AAC AAG ACG  | 290 |
| Pro Phe Thr Arg Ala Xaa Glu Glu Glu Arg Arg Arg Xaa Asn Lys Thr  |     |
| -30 -25 -20                                                      |     |
| ACC CTC ACT TAC GTG GCC GCT GTC GCC GTG GGC ATG CTN NGG GCG TCC  | 338 |
| Thr Leu Thr Tyr Val Ala Ala Val Ala Val Gly Met Leu Xaa Ala Ser  |     |
| -15 -10 -5                                                       |     |

TAC GCT GCC GTA  
Tyr Ala Ala Val  
1

350

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..186  
id W32758  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 132..248
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq SDPLCVLFLNTSG/QQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

AAATCCCTGC GGTCCCAGCG TCGCTCCGGA CGCTGCCAAC CTGTTCTCCA CCGTCGCTCG 60
ACTTCCACCT CTAAGACTCC CACGAAACTC AGGTTGAATA ATTCAFCAA TTACACAAC 120
GAACTCAAGA C ATG GCT GCC CAG TGT GTC ACA AAG GTG GCG CTG AAT GTT 170
 Met Ala Ala Gln Cys Val Thr Lys Val Ala Leu Asn Val
 -35 -30

TCC TGT GCC AAT CTT TTG GAT AAA GAT ATA GGG TCA AAG TCA GAC CCT 218
Ser Cys Ala Asn Leu Leu Asp Lys Asp Ile Gly Ser Lys Ser Asp Pro
-25 -20 -15

TTA TGT GTG TTA TTT TTG AAT ACA AGT GGT CAA CAG TGG TAT GAG GTT 266
Leu Cys Val Leu Phe Leu Asn Thr Ser Gly Gln Gln Trp Tyr Glu Val
-10 -5 1 5

GAG CGC ACA GAA AGG ATT AAG AAT TGC TTG AAT CCC CAA TTT TCC AAG 314
Glu Arg Thr Glu Arg Ile Lys Asn Cys Leu Asn Pro Gln Phe Ser Lys
 10 15 20

```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACA TTT ATT ATT GAT TAC TAC TTT GAA GTG GTT CAG AAA TTG AAA TTT | 362 |
| Thr Phe Ile Ile Asp Tyr Tyr Phe Glu Val Val Gln Lys Leu Lys Phe |     |
| 25 30 35                                                        |     |
| GGG GTT TAT GAC ATC GRC AAC AAA ACT ATT GAG CTG AGT GAT GAT GAC | 410 |
| Gly Val Tyr Asp Ile Xaa Asn Lys Thr Ile Glu Leu Ser Asp Asp Asp |     |
| 40 45 50                                                        |     |
| TTC TTA GGG                                                     | 419 |
| Phe Leu Gly                                                     |     |
| 55                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 35..374  
id W79829  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..301  
id H81957  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 373..404
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 298..329  
id H81957  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99



region 2..316  
id H62624  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 85..294  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq AVLDCAFYDPHTA/WS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

AAGTGTCTCTG AGGGAAGCAA GGAGGCGGCG GCGGCCGCAG CGAGTGGCGA GTAGTGGAAA 60
CGTTGCTTCTT GAGGGGAGCC CAAG ATG ACC GGT TCT AAC GAG TTC AAG CTG 111
 Met Thr Gly Ser Asn Glu Phe Lys Leu
 -70 -65

AAC CAG CCA CCC GAG GAT GGC ATC TCC TCC GTG AAG TTC AGC CCC AAC 159
Asn Gln Pro Pro Glu Asp Gly Ile Ser Ser Val Lys Phe Ser Pro Asn
-60 -55 -50

ACC TCC CAG TTC CTG CTT GTC TCC TCC TGG GAC ACG TCC GTG CGT CTC 207
Thr Ser Gln Phe Leu Leu Val Ser Ser Trp Asp Thr Ser Val Arg Leu
-45 -40 -35 -30

TAC GAT GTG CCG GCC AAC TCC ATG CGG CTC AAG TAC CAG CAC ACC GGC 255
Tyr Asp Val Pro Ala Asn Ser Met Arg Leu Lys Tyr Gln His Thr Gly
-25 -20 -15

GCC GTC CTG GAC TGC GCC TTC TAC GAT CCA ACG CAT GCC TGG AGT GGA 303
Ala Val Leu Asp Cys Ala Phe Tyr Asp Pro Thr His Ala Trp Ser Gly
-10 -5 1

GGA CTA GAT CAT CMV KTG AAA ATG CAT GAT TTG AAC ACT GAT CAA GAA 351
Gly Leu Asp His Xaa Xaa Lys Met His Asp Leu Asn Thr Asp Gln Glu
5 10 15

AAT CTT GTT GGG ACC CAT GAT GCC CCT ATC AGA TGT GTT GAA TAC TGT 399
Asn Leu Val Gly Thr His Asp Ala Pro Ile Arg Cys Val Glu Tyr Cys
20 25 30 35

CCA AGT
Pro Ser
405

```

## (2) INFORMATION FOR SEQ ID NO: 111:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 48..365  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 1..318  
                           id N31699  
                           est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 365..420  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 319..374  
                           id N31699  
                           est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 299..373  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
                           seq AHLWCWCGSHCCST/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

AGTGTTCCT CAAATGGCGG TGTGAAGAGA GTTCGCCTGA GCCAGATCCC AGGTTTCACT 60
GAAGAACTT CTTAGAGATT CATTGCACTT CTGAGATTTA ATGTTTACAA CTTGGAGTTG 120
TCGACCTTCT TATAAGATAC ATTTTGAAG TCAAATGAA AGTTTCTGT GAAGTTTGTAG 180
AAGAGTTATA CAAGAAGGTA CTTCTTGGAG CCACACTTGA AAATGACAGC CATGATTACG 240
TCTTTTATCT CAACCCAGCA GTTTCAGATC AAGATTGTTT TACAGCCACC TCCTTAGA 298
ATG GGC AAA CAC CTG TGG TAT CCA GGG CAG GCA TCA GCC CAT CTC TGT 346
Met Gly Lys His Leu Trp Tyr Pro Gly Gln Ala Ser Ala His Leu Cys
-25 -20 -15 -10

TGG TGT GGC TCC CAT TGC TGT AGC ACC TGT GTG TTT GAA GAC CAA CTC 394
Trp Cys Gly Ser His Cys Cys Ser Thr Cys Val Phe Glu Asp Gln Leu
 -5 1 5

TCA GAT GAG CGG TTC CAG AGA AGT AAT GCT CCT TCA GTT AAC AGT GAT 442
Ser Asp Glu Arg Phe Gln Arg Ser Asn Ala Pro Ser Val Asn Ser Asp
 10 15 20

```

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 81..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 3..308  
id T23663  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 81..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 3..308  
id T23653  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..297  
id T03538  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..217  
id H28147  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 356..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 233..263  
id H28147  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 144..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..225  
id R71352  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 173..211
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq MLAVSLTVXLLGA/MM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

AGTGAGGTGG TTTCTGCGGG TGAGGCTGGC GCCCGTACCA TGAGCGAGGC GGACGGGCTG 60
CGACAGCGCC GGGCCCTGCG GCCCGCAAGT CGTCACAGAC GATGATGGCC AGGCCCCGGA 120
GGCTAAGGAC GGCAGCTCCT TTAGCGGCAG AGTTTTCCGA GTGACCTTCT TG ATG CTG 178
 Met Leu

GCT GTT TCT CTC ACC GTT CBC CTG CTT GGA GCC ATG ATG CTG CTG GAA 226
Ala Val Ser Leu Thr Val Xaa Leu Leu Gly Ala Met Met Leu Leu Glu
 -10 -5 1 5

TCT CCT ATA GAT CCA CAG CCT CTC AGC TTC AAA GAA CCC CCG CTC TTG 274
Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro Leu Leu
 10 15 20

CTT GGT GTT CTG CAT CCA AAT ACG AAG CTG CGA CAG GCA GAA AGG CTG 322
Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu Arg Leu
 25 30 35

TTT GAA AAT CAA CTT GTT GGA CCG GAG TCC ATA GCA CAT ATT GGG GAT 370
Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile Gly Asp
 40 45 50

GTG ATG TTT ACT GGG AGC TGG 391
Val Met Phe Thr Gly Ser Trp
 55 60

```

## (2) INFORMATION FOR SEQ ID NO: 113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 76..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..128  
id R57344

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 204..235  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 128..159  
 id R57344  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 82..309  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
 seq MLELDLLVFHLWG/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

AAGTAGCGCC TGCWGGCGGY GGCAGTTTGC CCGCGGRWGT GTGAAGGGAG ACAGTGTGGA 60
GGCCACAGGG TACTCGCCAC G ATG AGC AGC ACC TTA GCT AAG ATC GCG GAG 111
 Met Ser Ser Thr Leu Ala Lys Ile Ala Glu
 -75 -70

ATA GAA GCA GAG ATG GCT CGG ACT CAA AAG AAC AAG GCC ACA GCA CAC 159
Ile Glu Ala Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Ala His
-65 -60 -55

CAC TTA GGG CTG CTT AAG GCT CGT CTT GCT AAG CTT CGT CGA GAA CTC 207
His Leu Gly Leu Leu Lys Ala Arg Leu Ala Lys Leu Arg Arg Glu Leu
-50 -45 -40 -35

ATT ACT CCA AAG GGT GGT GGT GGT GGA GGT CCA GGA GAA GGT TTT GAT 255
Ile Thr Pro Lys Gly Gly Gly Gly Gly Gly Pro Gly Glu Gly Phe Asp
-30 -25 -20

TGG CCA AGA CAG GTG ATG CTC GAA TTG GAT TTG TTG GTT TTC CAT CTG 303
Trp Pro Arg Gln Val Met Leu Glu Leu Asp Leu Leu Val Phe His Leu
-15 -10 -5

TGG GGA AGT CAA CAC TGC TTA GTA ACC TGG CAA GGG 339
Trp Gly Ser Gln His Cys Leu Val Thr Trp Gln Gly
 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 114:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..214  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..198  
id C18087  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..89  
id T73970  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 128..214  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 76..162  
id T73970  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 93..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 44..91  
id T73946  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..142  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 13..95  
id AA096472  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 144..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 96..125  
id AA096472  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 169..214  
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..46  
id AA280423  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 47..181  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 13.9  
seq LVLALLLVSAALS/SV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```
ATGGCGTAGA GCCTAGCAAC AGCGCAGGCT CCCAGCCGAG TCCGTT ATG GCC GCT 55
 Met Ala Ala
 -45

GCC GTC CCG AAG AGG ATG AGG GGG CCA GCA CAA GCG AAA CTG CTG CCC 103
Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro
-40 -35 -30

GGG TCG GCC ATC CAA GCC CTT GTG GGG TTG GCG CGG CCG CTG GTC TTG 151
Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro Leu Val Leu
-25 -20 -15

GCG CTC CTG CTT GTG TCC GCC GCT CTA TCC AGT GTT GTA TCA CGG ACT 199
Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val Ser Arg Thr
-10 -5 1 5

GAT TCA CCG AGC CCA CTG 217
Asp Ser Pro Ser Pro Leu
10
```

## (2) INFORMATION FOR SEQ ID NO: 115:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 147..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 152..269  
id AA015703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 316..366  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
 region 322..372  
 id AA015703  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 257..302  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 261..306  
 id AA015703  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 184..258  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 13.9  
 seq LLSLLFLVQGAHG/RG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

AACAAAGAGT TGGCAGATCA CGGATGGAGG GCAGCATCTC CCAACAGCCT GGGCGGCCGC 60
TGAGACCCAG AGAACCCAAG GACTCCCCTK GGGGGYWCA Y CCAGCAGCCT CTGCTTCCCA 120
GGAGAGAGGT GCTGAAGTCC ACGAAGAGGT GGTGACTTCC AAGAGTGACT CCGTCGGAGG 180
AAA ATG ACT CCC CAG TCG CTG CTG CAG ACG ACA CTG TTC CTG CTG AGT 228
 Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser
 -25 -20 -15

CTG CTC TTC CTG GTC CAA GGT GCC CAC GGC AGG GGC CAC AGG GAA GAC 276
Leu Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp
 -10 -5 1 5

TTT CGC TTC TGC AGC CAG CGG AAC CAG ACA CAC AGG AGC AGC CTC CAC 324
Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His
 10 15 20

TAY AAA CCC ACA CCA GAM CTG CGC ATC TCC ATC GAG AAC TCC GAA GAG 372
Tyr Lys Pro Thr Pro Xaa Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu
 25 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 116:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 43..397  
id W31335  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..34
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 10..42  
id W31335  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(151..440)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 64..353  
id N30852  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(82..157)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 348..423  
id N30852  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 51..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..264  
id HSPD03622  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 311..375
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 262..326  
id HSPD03622  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 389..434  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 342..387  
id HSPD03622  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..316  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 9..323  
id AA055130  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 316..375  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 324..383  
id AA055130  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 145..436  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 123..414  
id H19862  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 50..110  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 26..86  
id H19862  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 107..145  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 84..122  
id H19862  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..322  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11.6  
seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

AACCCGGTTC AGCTCGCCTT TCTTGGCCAG AGGCGCCGGT TGGACTCACG GCGGGGGC 58
ATG ATG GTG GTG GGT ACG GGC ACC TCG CTG GCG CTC TCC TCC CTC CTG 106
Met Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu
 -85 -80 -75

TCC CTG CTG CTC TTT GCT GGG ATG CAG ATT TAC AGC CGT CAG CTG GCC 154
Ser Leu Leu Leu Phe Ala Gly Met Gln Ile Tyr Ser Arg Gln Leu Ala
 -70 -65 -60

TCC ACC GAG TGG CTC ACC ATC CAG GGC GGC CTG CTT GGT TCG GGT CTC 202
Ser Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu
 -55 -50 -45

TTC GTG TTC TCG CTC ACT GCC TTC AAT AAT CTG GAG AAT CTT GTC TTT 250
Phe Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe
 -40 -35 -30 -25

GGC AAA GGA TTC CAA GCA AAG ATC TTC CCT GAG ATT CTC CTG TGC CTC 298
Gly Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu
 -20 -15 -10

CTG TTG GCT CTC TTT GCA TCT GGC CTC ATC CAC CRA GTC TGT GTC ACC 346
Leu Leu Ala Leu Phe Ala Ser Gly Leu Ile His Xaa Val Cys Val Thr
 -5 1 5

ACC TGC TTC ATC TTC TCC AGG GTT GGT CTG TAC TAC ATC AAC AAG ATC 394
Thr Cys Phe Ile Phe Ser Arg Val Gly Leu Tyr Tyr Ile Asn Lys Ile
 10 15 20

TCC TCC ACC CTG TAC CAG GCA GCA GCT CCA GTC CTC ACA CCA GCC 439
Ser Ser Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala
 25 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..64  
id R86288  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 217..251  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 204..238  
                           id T29670  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 56..112  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 11.6  
                           seq VFCLLAVAPGAHS/QE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ATCCAACAAC CACATCCCTT CTCTACAGAA GCCTCTGAGA AGAAAGTTCT TCACC ATG | 58  |
| Met                                                              |     |
| GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCT CCA GGT GCT  | 106 |
| Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly Ala  |     |
| -15 -10 -5                                                       |     |
| CAC TCC CAG GAA CAA CTG GTG CAG TCT GGG GCT GAG GTG TTG AAG CCT  | 154 |
| His Ser Gln Glu Gln Leu Val Gln Ser Gly Ala Glu Val Leu Lys Pro  |     |
| 1 5 10                                                           |     |
| GGG GCC TCA GTG AAC ATT TCC TGC AGG GCA TCT GGG TTC ACC TTC ACC  | 202 |
| Gly Ala Ser Val Asn Ile Ser Cys Arg Ala Ser Gly Phe Thr Phe Thr  |     |
| 15 20 25 30                                                      |     |
| AAT TAT TAT GTG CAC TGG GTG CGA CAG GCC CCT GGA CAC GGG CTT GAG  | 250 |
| Asn Tyr Tyr Val His Trp Val Arg Gln Ala Pro Gly His Gly Leu Glu  |     |
| 35 40 45                                                         |     |
| TGG ATG GGA GTG ATC AAC CCC GTT AGT GGT TAC ACA AGT TAC GCA CAG  | 298 |
| Trp Met Gly Val Ile Asn Pro Val Ser Gly Tyr Thr Ser Tyr Ala Gln  |     |
| 50 55 60                                                         |     |
| AAA CTG CAG GGC AGA CTG ACC ATG ACC ACG GAC ACG GCC GCG AAT ATA  | 346 |
| Lys Leu Gln Gly Arg Leu Thr Met Thr Thr Asp Thr Ala Ala Asn Ile  |     |
| 65 70 75                                                         |     |
| GTC TAC ATG GAC CTC AGT AGG CTG AAA TCT GAC GAC ACG GCC GTG TAT  | 394 |
| Val Tyr Met Asp Leu Ser Arg Leu Lys Ser Asp Asp Thr Ala Val Tyr  |     |
| 80 85 90                                                         |     |
| TTC TGT GCG AAA GTG CGG TGT CTT AAG GGG ATA TGC TAT ACA GAG GAT  | 442 |
| Phe Cys Ala Lys Val Arg Cys Leu Lys Gly Ile Cys Tyr Thr Glu Asp  |     |
| 95 100 105 110                                                   |     |
| GCT CTG GAT CTT TGG                                              | 457 |
| Ala Leu Asp Leu Trp                                              |     |
| 115                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 439 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Umbilical cord
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 75..429  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 43..397  
 id W31335  
 est
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 32..73  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 1..42  
 id W31335  
 est
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 33..355  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 1..323  
 id AA055130  
 est
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 355..414  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 324..383  
 id AA055130  
 est
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 56..384  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 28..356  
 id AA252648  
 est
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 385..428  
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 356..399  
id AA252648  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 113..439  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 38..364  
id AA228934  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 184..440  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 123..379  
id H19862  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 89..149  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 26..86  
id H19862  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 146..184  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 84..122  
id H19862  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 23..361  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11.6  
seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AAGTCCGCGG TAAGGCTGAC GC ATG CGC ATA GCT AAC CGC ACC CGG TTC AGC | 52  |
| Met Arg Ile Ala Asn Arg Thr Arg Phe Ser                          |     |
| -110 -105                                                        |     |
| TCG CCT TTC TTG GCC AGA GGC GCC GGT TGG ACT CAC GGG CGG GGC ATG  | 100 |
| Ser Pro Phe Leu Ala Arg Gly Ala Gly Trp Thr His Gly Arg Gly Met  |     |
| -100 -95 -90                                                     |     |
| ATG GTG GTG GGT ACG GGC ACC TCG CTG GCG CTC TSS TCC CTC CTG TCC  | 143 |
| Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Xaa Ser Leu Leu Ser  |     |

| -85                                                             | -80 | -75 |     |
|-----------------------------------------------------------------|-----|-----|-----|
| CTG CTG CTC TTT GCT GGG ATG CAG ATG TAC AGC CGT CAG CTG GCC TCC |     |     | 196 |
| Leu Leu Leu Phe Ala Gly Met Gln Met Tyr Ser Arg Gln Leu Ala Ser |     |     |     |
| -70                                                             | -65 | -60 |     |
| ACC GAG TGG CTC ACC ATC CAG GGC GGC CTG CTT GGT TCG GGT CTC TTC |     |     | 244 |
| Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe |     |     |     |
| -55                                                             | -50 | -45 | -40 |
| GTG TTC TCG CTC ACT GCC TTC AAT AAT CTG GAG AAT CTT GTC TTT GGC |     |     | 292 |
| Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe Gly |     |     |     |
| -35                                                             | -30 | -25 |     |
| AAA GGA TTC CAA GCA AAG ATC TTC CCT GAG ATT CTC CTG TGC CTC CTG |     |     | 340 |
| Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu |     |     |     |
| -20                                                             | -15 | -10 |     |
| TTG GCT CTC TTT GCA TCT GGC CTC ATC CAC CGA GTC TGT GTC ACC ACC |     |     | 388 |
| Leu Ala Leu Phe Ala Ser Gly Leu Ile His Arg Val Cys Val Thr Thr |     |     |     |
| -5                                                              | 1   | 5   |     |
| TGC TTC ATC TTC TCC ATG GTT GGT CTG TAC TAC ATC AAC AAG ATC TCC |     |     | 436 |
| Cys Phe Ile Phe Ser Met Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser |     |     |     |
| 10                                                              | 15  | 20  | 25  |
| TCC                                                             |     |     | 439 |
| Ser                                                             |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..235  
id AA280774  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 246..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 230..266  
id AA280774

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..259  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..243  
id HUM404F03B  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..282  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..263  
id W05476  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..282  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..262  
id R33542  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 12..282  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 8..278  
id T85491  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 151..222  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11.4  
seq LMSLLLVPVVEA/VE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```
ADTCCTGTAA TGGCTGCTTC CTAGAAGGTC GTGTCACGTG GAACCTCTTA ATCTCAGCAT 60
CCGGAGCTCC AGGAAGGGAA AATTTCAAGT CAGATAGAAT TCTATATATA CCATTTCTTT 120
GGAACCTTCA GCCCTCAAGA TTCCAACATC ATG ACC TCA GTT TCA ACA CAG TTG 174
 Met Thr Ser Val Ser Thr Gln Leu
 -20
TCC TTA GTC CTC ATG TCA CTG CTT TTG GTG CTG CCT GTT GTG GAA GCA 222
Ser Leu Val Leu Met Ser Leu Leu Leu Val Leu Pro Val Val Glu Ala
-15 -10 -5
GTA GAA GCC GGT GAT GCA ATC GCC CTT TTG TTA GGT GTG GTT CTC AGC 270
```



Val Glu Ala Gly Asp Ala Ile Ala Leu Leu Leu Gly Val Val Leu Ser  
1 5 10 15  
ATT ACA GGC ATT GTG CCT GCT TGG GGG TAT ATG CAY GGG  
Ile Thr Gly Ile Val Pro Ala Trp Gly Tyr Met His Gly  
20 25

309

## (2) INFORMATION FOR SEQ ID NO: 120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..363
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 60..328  
id H19572  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 106..256  
id H46195  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..148
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 62..115  
id H46195  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(207..316)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 183..292  
id H46196  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(314..363)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 137..186  
id H46196  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(172..212)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 288..328  
id H46196  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(237..287)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 239..289  
id H19490  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(284..317)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 208..241  
id H19490  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(331..363)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 160..192  
id H19490  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 263..322  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11.2  
seq ILVVLMLPLAQA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AAGACACGCC TACGATTAGA CTCAGGCAGG CACCTACCGG CGAGCGGCCG CRVGTGACTC 60  
CCAGGCGCGG CGGTACCTCA CGGTGGTGAA GGTACAGGG TTGCAGCACT CCCAGTAGAC 120  
CAGGAGCTCC GGGAGGCAGG GCCGGCCCCA CGTCCTCTGC GCACCACCCT GAGTTGGATC 180  
CTCTGTGCGC CACCCCTGAG TTGGATCCAG GGCTAGCTGC TGTTGACCTC CCCACTCCCA 240

```
CGCTGCCCTC CTGCCTGCAG CC ATG ACG CCC CTG CTC ACC CTG ATC CTG GTG 292
 Met Thr Pro Leu Leu Thr Leu Ile Leu Val
 -20 -15

GTC CTC ATG GGC TTA CCT CTG GCC CAG GCC TTG GAC TGC CAC GTG TGT 340
Val Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys
-10 -5 1 5

NCC TAC AAC GGA GAC AAC TGC 361
Xaa Tyr Asn Gly Asp Asn Cys
 10
```

## (2) INFORMATION FOR SEQ ID NO: 121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..372
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..353  
id W05519  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 368..423
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 348..403  
id W05519  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..260
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 21..264  
id T97490  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 231..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 287..347

id T97490  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 16..315  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..300  
id HUML12811  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 16..275  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..260  
id HUML13801  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 139..186  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11  
seq LLALSLLVLWTSP/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

|     |     |      |      |      |     |      |      |     |      |       |     |     |      |      |      |      |     |
|-----|-----|------|------|------|-----|------|------|-----|------|-------|-----|-----|------|------|------|------|-----|
| AAT | CCC | CAGC | CTC  | ACAT | CAC | TCAC | ACCT | TG  | CATT | TACCC | CTG | CAT | CCCA | GTG  | CCC  | CTGC | 60  |
| AGC | CTC | CAC  | AC   | AGAT | CCT | GCA  | CAC  | ACC | CAGA | CAG   | CTG | GGC | GC   | TCAC | ACAT | TTC  | 120 |
| TGC | CTC | TGTT | CACC | CTCC | ATG | GCC  | CTG  | CTA | CTG  | GCC   | CTC | AGC | CTG  | CTA  | GTT  |      | 171 |
|     |     |      |      |      | Met | Ala  | Leu  | Leu | Leu  | Ala   | Leu | Ser | Leu  | Leu  | Val  |      |     |
|     |     |      |      |      | -15 |      |      |     |      |       |     |     |      |      |      | -10  |     |
| CTC | TGG | ACT  | TCC  | CCA  | GCC | CCA  | ACT  | CTG | AGT  | GGC   | ACC | AAT | GAT  | GCT  | GAA  |      | 219 |
| Leu | Trp | Thr  | Ser  | Pro  | Ala | Pro  | Thr  | Leu | Ser  | Gly   | Thr | Asn | Asp  | Ala  | Glu  |      |     |
| -5  |     |      |      |      | 1   |      |      |     | 5    |       |     |     |      | 10   |      |      |     |
| GAC | TGC | TGC  | CTG  | TCT  | GTG | ACC  | CAG  | AAA | CCC  | ATC   | CCT | GGG | TAC  | ATC  | GTG  |      | 267 |
| Asp | Cys | Cys  | Leu  | Ser  | Val | Thr  | Gln  | Lys | Pro  | Ile   | Pro | Gly | Tyr  | Ile  | Val  |      |     |
|     |     |      | 15   |      |     |      |      | 20  |      |       |     |     | 25   |      |      |      |     |
| AGG | AAC | TTC  | CAC  | TAC  | CTT | CTC  | ATC  | AAG | GAT  | GGC   | TGC | AGG | GTG  | CCT  | GCT  |      | 315 |
| Arg | Asn | Phe  | His  | Tyr  | Leu | Leu  | Ile  | Lys | Asp  | Gly   | Cys | Arg | Val  | Pro  | Ala  |      |     |
|     | 30  |      |      |      |     |      | 35   |     |      |       |     | 40  |      |      |      |      |     |
| GTA | GTG | TTC  | ACC  | ACA  | CTG | AGG  | GGC  | CGC | CAG  | CTC   | TGT | GCA | CCC  | CCA  | GAC  |      | 363 |
| Val | Val | Phe  | Thr  | Thr  | Leu | Arg  | Gly  | Arg | Gln  | Leu   | Cys | Ala | Pro  | Pro  | Asp  |      |     |
|     | 45  |      |      |      |     | 50   |      |     |      |       | 55  |     |      |      |      |      |     |
| CAG | CCC | TGG  | GTA  | GAA  | CGC | ATC  | ATC  | CAG | AGA  | CTG   | CAG | AGG | ACC  | TCA  | GCC  |      | 411 |
| Gln | Pro | Trp  | Val  | Glu  | Arg | Ile  | Ile  | Gln | Arg  | Leu   | Gln | Arg | Thr  | Ser  | Ala  |      |     |
| 60  |     |      |      |      | 65  |      |      |     | 70   |       |     |     |      | 75   |      |      |     |
| AAG | ATG | AAR  | MGC  | CGM  | AGC | AGT  | KAA  | CCT | ATG  | AMC   | GTG | MAG | AGG  | GAR  | CCG  |      | 459 |
| Lys | Met | Lys  | Xaa  | Arg  | Ser | Ser  | Xaa  | Pro | Met  | Xaa   | Val | Xaa | Arg  | Glu  | Pro  |      |     |

|                                                                 | 80 |   | 85  |  | 90  |     |
|-----------------------------------------------------------------|----|---|-----|--|-----|-----|
| GAG TCC GAG TCA AGC ATT GTG AAT KAT TAC CTA MCT GGG GAA CGA RGA |    |   |     |  |     | 507 |
| Glu Ser Glu Ser Ser Ile Val Asn Xaa Tyr Leu Xaa Gly Glu Arg Xaa |    |   |     |  |     |     |
|                                                                 | 95 | * | 100 |  | 105 |     |
| AGG                                                             |    |   |     |  |     | 510 |
| Arg                                                             |    |   |     |  |     |     |

## (2) INFORMATION FOR SEQ ID NO: 122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 152..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 91..226  
id W60940  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..160
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 48..100  
id W60940  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..106
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..47  
id W60940  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 152..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 90..254  
id H39980  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..160
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..99  
id H39980  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 308..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 247..323  
id H39980  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(148..292)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 282..426  
id N41026  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(283..384)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 191..292  
id N41026  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..160
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 8..102  
id R49793  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 199..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 141..213  
id R49793  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 152..199
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 93..140  
id R49793

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 18..160  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..143  
                           id W74783  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 190..253  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 173..236  
                           id W74783  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 74..136  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.5  
                           seq RLLLLPLLLAVSG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

AATTTCACTT GCCTGGACGC TGCGCCACAT CCCACCGGCC CTTACACTGT GGTGTCCAGC 60
AGCATCCGGC TTC ATG GGG GGA CTT GAA CCC TGC AGC AGG CTC CTG CTC 109
 Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu
 -20 -15 -10

CTG CCT CTC CTG CTG GCT GTA AGT GGT CTC CGT CCT GTC CAG GCC CAG 157
Leu Pro Leu Leu Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln
 -5 1 5

GCC CAG AGC GAT TGC AGT TGC TCT ACG GTG AGC CCG GGC GTG CTG GCA 205
Ala Gln Ser Asp Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala
 10 15 20

GGG ATC GTG ATG GGA GAC CTG GTG CTG ACA GTG CTC ATT GCC CTG GCC 253
Gly Ile Val Met Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala
 25 30 35

GTG TAC TTC CTG GGC CGG CTG GTC CCT CGG GGG CGA GGG GCT GCG GAG 301
Val Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu
 40 45 50 55

GCA SNG ACC CGG AAA CAG CGT ATC ACT GAG ACC GGG TCG CCT TAT CAG 349
Ala Xaa Thr Arg Lys Gln Arg Ile Thr Glu Thr Gly Ser Pro Tyr Gln
 60 65 70

GAG CTC CAG GGT CAG AGG TCG GAT GTC TAC AGC 382
Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser
 75 80

```

## (2) INFORMATION FOR SEQ ID NO: 123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..196
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 13..155  
id N41450  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 153..292  
id N41450  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 327..425
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 288..386  
id N41450  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 202..330  
id W76359  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 54..124  
id W76359  
est



## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 3..54  
id W76359  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 327..370
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 326..369  
id W76359  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..196
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 162..194  
id W76359  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..163
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 132..162  
id W76359  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 46..120  
id W04321  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..47  
id W04321  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 153..190  
id W04321

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..163
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 115..153  
id W04321  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 12..134  
id AA025985  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 208..294  
id AA025985  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 366..425
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 381..440  
id AA025985  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..166
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 145..176  
id AA025985  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 208..306
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 146..244  
id H09017  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..126
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..65  
id H09017  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 327..368  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 267..308  
id H09017  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 178..249  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10  
seq LCRALCLFPRVFA/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```
AAAGGACTCC AAAGCGAGGC CGGGGACTGA AGGTGTGGGT GTCGAGCCCT CTGGCAGAGG 60
GTTAACCTGG GTCAAATGCA CGGATTCTCA CCTCGTACAG TTACGCTCTC CCGCGGCACG 120
TCCGCGAGGA CTTGAAGTCC TGAGCGCTCA AGTTTGTCCG TAGGTCGAGA GAAGGCC 177
ATG GAG GTG CCG CCA CCG GCA CCG CGG AGC TTT CTC TGT AGA GCA TTG 225
Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
 -20 -15 -10
TGC CTA TTT CCC CGA GTC TTT GCT GCC GAA GCT GTG ACT GCC GAT TCG 273
Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
 -5 1 5
GPA GTC CTT GAG GAG CGT CAG AAG CGG CTT CCC TAC STC CCA GAG CCC 321
Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Xaa Pro Glu Pro
 10 15 20
TAT TAC CGG AAT CTG GAT GGG ACC GCC TCC GGG AGC TGT TTK GCA AAG 369
Tyr Tyr Arg Asn Leu Asp Gly Thr Ala Ser Gly Ser Cys Xaa Ala Lys
 25 30 35
ATG AAC AGC AGA GAA TTT CAA AGG ACC TTG CTA ATA TCT GTA AGA CGG 417
Met Asn Ser Arg Glu Phe Gln Arg Thr Leu Leu Ile Ser Val Arg Arg
 45 50 55
CAG CTA
Gln Leu 423
```

## (2) INFORMATION FOR SEQ ID NO: 124:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 8..208  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 1..201  
                            id N56128  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 242..311  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 94  
                            region 233..302  
                            id N56128  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 207..244  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 94  
                            region 199..236  
                            id N56128  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 19..113  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 1..95  
                            id N87312  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 223..286  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 90  
                            region 208..271  
                            id N87312  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 181..222  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 92  
                            region 165..206  
                            id N87312  
                            est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 46..270  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 1..225  
 id R57616  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 51..241  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 1..191  
 id AA093451  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 75..131  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.5  
 seq LMCLSLCTAFALS/KP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

AGAGCTGAGC CGGTGGGTGA GCGGCGGCCA CGGCATCCTG TGCTGTGGGG GCTACGAGGA 60
AAGATCTAAT TATC ATG GAC CTG CGA CAG TTT CTT ATG TGC CTG TCC CTG 110
 Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu
 -15 -10

TGC ACA GCC TTT GCC TTG AGC AAA CCC ACA GAA AAG AAG GAC CGT GTA 158
Cys Thr Ala Phe Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val
 -5 1 5

CAT CAT GAG CCT CAG CTC AGT GAC AAG GTT CAC AAT GAT GCT CAG AGT 206
His His Glu Pro Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser
 10 15 20 25

TTT GWT TAT GAC CAT GAT GCC TTC TTG GGT GCT GAA GAA GCA AAG ASM 254
Phe Xaa Tyr Asp His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Xaa
 30 35 40

TTT GAT CAG CTG ACA CCA GAA GAG AGC AAG GAA AGG CTT GGA AAG ATT 302
Phe Asp Gln Leu Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile
 45 50 55

GTA AGT AAR ATM GAT GGC GAC AAG GAC GGG TTT GTC ACT GTG GAT GAG 350
Val Ser Lys Ile Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu
 60 65 70

CTC AAA
Leu Lys
 75

```

## .2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 320 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Substantia nigra
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 50..320  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 17..287  
                            id R35366  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 42..320  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 10..288  
                            id R35909  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 42..318  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 10..286  
                            id R20566  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 42..320  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 10..288  
                            id H09254  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 42..320  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 10..288  
                            id R25274  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: 24..113

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.5  
seq LLFLSQFCILSGG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

AAAAGTGC GC AGGCGCTGGC AAG ATG GCG GGA GGG GTG CGC CCG CTG CGG GGC 53
 Met Ala Gly Gly Val Arg Pro Leu Arg Gly
 -30 -25

CTC CGC GCC TTG TGT CGC GTG CTG CTC TTC CTC TCG CAG TTC TGC ATT 101
Leu Arg Ala Leu Cys Arg Val Leu Leu Phe Leu Ser Gln Phe Cys Ile
-20 -15 -10 -5

CTG TCG GGC GGT GAA AGT ACT GAA ATC CCA CCT TAT GTG ATG AAG TGT 149
Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys Cys
 1 5 10

CCG AGC AAT GGT TTG TGT AGC AGG CTT CCT GCA GAC TGT ATA GAC AGC 197
Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp Ser
 15 20 25

ACA ACA AAT TTC TCC TGT ACC TAT GGG AAG CCT GTM ACT TTT GAC TGT 245
Thr Thr Asn Phe Ser Cys Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys
 30 35 40

RCA GTG AAA CCA TCT GTT ACC TGT GTT GAT CAA GAC TTC AAA TCC CAA 293
Xaa Val Lys Pro Ser Val Thr Cys Val Asp Gln Asp Phe Lys Ser Gln
 45 50 55 60

AAG RAC TTC ATC ATT AAC ATG ACT TGC 320
Lys Xaa Phe Ile Ile Asn Met Thr Cys
 65

```

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..198)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 2..198  
id N27605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(2..69)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..68  
                           id N78549  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 36..98  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.3  
                           seq VLPVILLLLGAHP/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAATGCTTT CGGTAGGCAC TCCAMGGCTG TRAAG ATG GCG GCG GCT GCG TGG  | 53  |
| Met Ala Ala Ala Ala Trp                                         |     |
| -20                                                             |     |
| CTT CAG GTG TTG CCT GTC ATT CTT CTG CTT CTG GGA GCT CAC CCG TCA | 101 |
| Leu Gln Val Leu Pro Val Ile Leu Leu Leu Leu Gly Ala His Pro Ser |     |
| -15 -10 -5 1                                                    |     |
| CCA CTG TCG TTT TTC AGT GCG GGA CCG GCA ACC GTA GCT GCT GCC GAC | 149 |
| Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala Thr Val Ala Ala Ala Asp |     |
| 5 10 15                                                         |     |
| CGG TCC AAA TGG CAC ATT CCG ATA CCG TCG GGG AAA AAT TAT TTT AGT | 197 |
| Arg Ser Lys Trp His Ile Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser |     |
| 20 25 30                                                        |     |
| TTT GGA AHK ATC CTC TTC AGA AAT ACC ACT ATC TTC CTG AAG TTT GAT | 245 |
| Phe Gly Xaa Ile Leu Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp |     |
| 35 40 45                                                        |     |
| GGA GAA CCT TGT GAC CTG TCT TTG AAT ATA AYM TGG TAT CTG AAA AGC | 293 |
| Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile Xaa Trp Tyr Leu Lys Ser |     |
| 50 55 60 65                                                     |     |
| GCT GAT TGT TAC AAT GAA ATC TAT AAC TTC AAG GCA GAA GAA GTA GAG | 341 |
| Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe Lys Ala Glu Glu Val Glu |     |
| 70 75 80                                                        |     |
| TTG TAT TTG GAA AAA CTT AAG GAA AAA AGA GGC TTG TCT GGG AAA TGG | 389 |
| Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg Gly Leu Ser Gly Lys Trp |     |
| 85 90 95                                                        |     |

## (x) INFORMATION FOR SEQ ID NO: 127:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..267  
id HSC1WH101  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 134..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 41..204  
id R12437  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..136
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..42  
id R12437  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..203  
id R13448  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 244..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 82..135  
id T69236  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 197..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 36..83  
id T69236  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: 212..268  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.3  
 seq LLWLALACSPVHT/XL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ATCCGGCGCG CTGGAGCGTT TTCCGGCCGT GCGTTTGTGG CCGTCCGGCC TCCCTGACAT 60
GCAGATTTCC ANSSAGAAGA CAGAGAAGGA GCNAGTGGTC ATGGAATGGG CTGGGGTCAA 120
AGACTGGGTG CCTGGGAGCT GAGGCAGCCA CCGTTTCAGC CTGGCCAGCC CTCTGGACCC 180
CGAGGTTGGA CCCTACTGTG ACACACCTAC C ATG CGG ACA CTC TTC AAC CTC 232
 Met Arg Thr Leu Phe Asn Leu
 -15
CTC TGG CTT GCC CTG GCC TGC AGC CCT GTT CAC ACT ASC CTG TCA AAG 280
Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Xaa Leu Ser Lys
 -10 -5 1
TCA GAT GCC VSA AAA CCG CCT AGG 304
Ser Asp Ala Xaa Lys Pro Pro Arg
 5 10

```

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 216 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 43..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 29..148  
                           id T98462  
                           est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 179..216  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 165..202  
                           id T98462  
                           est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..162  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 110..255  
id T82829  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 16..162  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..147  
id AA027213  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 32..162  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 2..132  
id AA095731  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 179..216  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 149..186  
id AA095731  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(85..162)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 358..435  
id AA027214  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(16..87)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 434..505  
id AA027214  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 37..84  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.3  
seq LFVAIFAVPLILG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

CTTTTTTACT TTCACAGCAA TAGTGCAGAA TCCAGA ATG GAT GTC CTC TTT GTA 54
 Met Asp Val Leu Phe Val
 -15

GCC ATC TTT GCT GTG CCA CTT ATC CTG GGA CAA GAA TAT GAG GAT GAA 102
Ala Ile Phe Ala Val Pro Leu Ile Leu Gly Gln Glu Tyr Glu Asp Glu
-10 -5 1 5

GAA AGA CTG GGA GAG GAT GAA TAT TAT CAG GTG GTC TAT TAT TAT ACA 150
Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln Val Val Tyr Tyr Tyr Thr
 10 15 20

GTC ACC CCC ATT ATG ATG RCY TTA GGG MCR RAT TTC ACC ATT GAT TAC 198
Val Thr Pro Ile Met Met Xaa Leu Gly Xaa Xaa Phe Thr Ile Asp Tyr
 25 30 35

KCC ATA TTT GAG TCA GAG 216
Xaa Ile Phe Glu Ser Glu
 40

```

## (2) INFORMATION FOR SEQ ID NO: 129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(3..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 3..181  
id N27605  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(3..53)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..51  
id N78549  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 20..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3

seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AAACTCCACG GCTGTGAAG ATG GCG GCT GCT GCG TGG CTT CAG GTG TTG CCT | 52  |
| Met Ala Ala Ala Trp Leu Gln Val Leu Pro                          |     |
| -20 -15                                                          |     |
| GTC ATT CTT CTG CTT CTG GGA GCT CAC CCG TCA CCA CTG TCG TTT TTC  | 100 |
| Val Ile Leu Leu Leu Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe  |     |
| -10 -5 1 5                                                       |     |
| AGT GCG GGA CCG GCA ACC GTA GCT GCT GCC GAC CGG TCC AAA TGG CAC  | 148 |
| Ser Ala Gly Pro Ala Thr Val Ala Ala Asp Arg Ser Lys Trp His      |     |
| 10 15 20                                                         |     |
| ATT CCG ATA CCG TCG GGG AAA AAT TAT TTT AGT TTT GGA AAG ATC CTC  | 196 |
| Ile Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu  |     |
| 25 30 35                                                         |     |
| TTC AGA AAT ACC ACT ATC TTC CTG AAG TTT GAT GGA GAA CCT TGT GAC  | 244 |
| Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp  |     |
| 40 45 50                                                         |     |
| CTG TCT TTG AAT ATA ACC TGG TAT CTG AAA AGC GCT GAT TGT TAC AAT  | 292 |
| Leu Ser Leu Asn Ile Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn  |     |
| 55 60 65 70                                                      |     |
| GAA ATC TAT AAC TTC AAG GCA GAA GAA GTA GAG TTG TAT TTG GAA AAA  | 340 |
| Glu Ile Tyr Asn Phe Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys  |     |
| 75 80 85                                                         |     |
| CTT                                                              | 343 |
| Leu                                                              |     |

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..243
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 72..267  
id R13448  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 126..255  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 82..211  
id T69236  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 79..126  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 36..83  
id T69236  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..244  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 73..269  
id R12437  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..211  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 136..299  
id HSC1WH101  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..50  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..34  
id HSC1WH101  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 94..150  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.2  
seq LLXLALACSPVHT/TL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AGCGTTTTCG GGCCTGCGT TTGTGGCCGT CCGGCCTCCC TGACATGCAG CCCTCTGGAC 60

CCCGAGGTTG GACCCTACTG TGACACACCT ACC ATG CGG ACA CTC TTC AAC CTC 114

Met Arg Thr Leu Phe Asn Leu

-15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTC | TKG | CTT | GCC | CTG | GCC | TGC | AGC | CCT | GTT | CAC | ACT | ACC | CTG | TCA | AAG | 162 |
| Leu | Xaa | Leu | Ala | Leu | Ala | Cys | Ser | Pro | Val | His | Thr | Thr | Leu | Ser | Lys |     |
|     |     | -10 |     |     |     |     | -5  |     |     |     |     |     | 1   |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TCA | GAT | GCC | AAA | AAA | GCC | GCC | TCA | AAG | ACG | CTG | CTG | GAG | AAG | AGT | CAG | 210 |
| Ser | Asp | Ala | Lys | Lys | Ala | Ala | Ser | Lys | Thr | Leu | Leu | Glu | Lys | Ser | Gln |     |
| 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     | 20  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TTT | TCA | GAT | AAG | CCG | GTG | CAA | GAC | CGG | GGT | TTG | GTG | GTG | ACG | GAC | GGG | 258 |
| Phe | Ser | Asp | Lys | Pro | Val | Gln | Asp | Arg | Gly | Leu | Val | Val | Thr | Asp | Gly |     |
|     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     | 35  |     |     |

## (2) INFORMATION FOR SEQ ID NO: 131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 8..198  
id R72126  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 8..175  
id W60037  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..174  
id W24729  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 228..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 209..252  
id W24729  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 18..191  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..174  
id R74426  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 228..271  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 209..252  
id R74426  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 18..191  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..174  
id H42031  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 228..271  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 209..252  
id H42031  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 62..181  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9  
seq LLCLLHFSIVSVA/AX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```
ACTGAAGTGG GCAAAATCCC CGAGAAGCAG CGGTGTCCCC AGCCTCTCAC TCGGAGCCGA 60
T ATG GGG AGT AAA GTG GCG GAC CTG CTG TAC TGG AAG GAC ACG AGG ACG 109
Met Gly Ser Lys Val Ala Asp Leu Leu Tyr Trp Lys Asp Thr Arg Thr
-40 -35 -30 -25

TCA GGA GTG GTC TTC ACA GGC CTG ATG GTC TCC CTC CTC TGC CTC CTG 157
Ser Gly Val Val Phe Thr Gly Leu Met Val Ser Leu Leu Cys Leu Leu
-20 -15 -10

CAC TTT AGC ATC GTG TCC GTG GCC GCG SAC TTT GGS YCK KKT DSY WGM 205
```



TGC ACC GGG GGG ATG GAG 271  
Cys Thr Gly Gly Met Glu  
25 30

(A) NAME/KEY: other  
(B) LOCATION: 35.229  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..195  
id AA206940

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 35..229  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..195  
id AA186993  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 37..229  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..193  
id T68050  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 32..178  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..147  
id AA157180  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 175..231  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 146..202  
id AA157180  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 28..114  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.9  
seq ALLIVCDVPSASA/QR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```
TCACCTTATAG AAGGGAGAGG AGCGAAC ATG GCA GCG CGT TGG CGG TTT TGG TGT 54
 Met Ala Ala Arg Trp Arg Phe Trp Cys
 -25

GTC TCT GTG ACC ATG GTG GTG GCG CTG CTC ATC GTT TGC GAC GTT CCC 102
Val Ser Val Thr Met Val Val Ala Leu Leu Ile Val Cys Asp Val Pro
-20 -15 -10 -5

TCA GCC TCT GCC CAA AGA AAG AAG GAG ATG GTG TTA TCT GAA AAG GTT 150
Ser Ala Ser Ala Gln Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val
 1 5 10

AGT CAG CTG ATG GAA TGG ACT AAC AAA AGA CCT GTA ATA AGA ATG AAT 198
```

Ser Gln Leu Met Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn  
15 20 25  
GGA GAC AAG TTC CGT CGC CTT GTG AAG CCC CAC ATG  
Gly Asp Lys Phe Arg Arg Leu Val Lys Pro His Met  
30 35 40

234

## (2) INFORMATION FOR SEQ ID NO: 133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 186..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..81  
id AA089592  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 266..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 81..127  
id AA089592  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 385..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 194..224  
id AA089592  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(305..440)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 211..346  
id R83736  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(294..439)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 202..347  
                           id R83667  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 30..86  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.8  
                           seq SAVLSGFVLGALA/FQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

|          |     |         |      |         |     |     |     |     |     |     |     |     |     |     |     |     |
|----------|-----|---------|------|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AACTCTTG | GTG | TAGCCTG | GAGG | CGGCGGT | AS  | ATG | GAG | GGG | GAG | AGT | ACG | TCG | GCG | 53  |     |     |
|          |     |         |      |         |     | Met | Glu | Gly | Glu | Ser | Thr | Ser | Ala |     |     |     |
|          |     |         |      |         |     |     |     |     |     |     |     |     |     | -15 |     |     |
| GTG      | CTC | TCG     | GGC  | TTT     | GTG | CTC | GGC | GCA | CTC | GCT | TTC | CAG | CAC | CTC | AAC | 101 |
| Val      | Leu | Ser     | Gly  | Phe     | Val | Leu | Gly | Ala | Leu | Ala | Phe | Gln | His | Leu | Asn |     |
|          | -10 |         |      |         |     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |
| ACG      | GAC | TCG     | GAC  | ACG     | GAA | GGT | TTT | CTT | CTT | GGG | GAA | GTA | AAA | GGT | GAA | 149 |
| Thr      | Asp | Ser     | Asp  | Thr     | Glu | Gly | Phe | Leu | Leu | Gly | Glu | Val | Lys | Gly | Glu |     |
|          |     |         |      | 10      |     |     |     | 15  |     |     |     |     |     | 20  |     |     |
| GCC      | AAG | AAC     | AGC  | ATT     | ACT | GAT | TCC | CAA | ATG | GAT | GAT | GTT | GAA | GTT | GTT | 197 |
| Ala      | Lys | Asn     | Ser  | Ile     | Thr | Asp | Ser | Gln | Met | Asp | Asp | Val | Glu | Val | Val |     |
|          |     |         | 25   |         |     |     |     | 30  |     |     |     |     | 35  |     |     |     |
| TAT      | ACA | ATT     | GAC  | ATT     | CAG | AAA | TAT | ATT | CCA | TGC | TAT | CAG | CTT | TTT | AGC | 245 |
| Tyr      | Thr | Ile     | Asp  | Ile     | Gln | Lys | Tyr | Ile | Pro | Cys | Tyr | Gln | Leu | Phe | Ser |     |
|          |     | 40      |      |         |     |     | 45  |     |     |     |     | 50  |     |     |     |     |
| TTT      | TAT | AAT     | TCT  | TCA     | GGC | GAA | GTA | AAT | GAG | CAA | GCA | CTG | AAG | AAA | ATA | 293 |
| Phe      | Tyr | Asn     | Ser  | Ser     | Gly | Glu | Val | Asn | Glu | Gln | Ala | Leu | Lys | Lys | Ile |     |
|          | 55  |         |      |         |     | 60  |     |     |     |     | 65  |     |     |     |     |     |
| TTA      | TCA | AAT     | GTC  | AAA     | AAG | AAT | GTG | GTA | GGT | TGG | TAC | AAA | TTC | CGT | CGT | 341 |
| Leu      | Ser | Asn     | Val  | Lys     | Lys | Asn | Val | Val | Gly | Trp | Tyr | Lys | Phe | Arg | Arg |     |
|          | 70  |         |      |         | 75  |     |     |     | 80  |     |     |     |     | 85  |     |     |
| CAT      | TCA | GAT     | CAG  | ATC     | ATG | ACG | TTT | AGA | GAG | AGG | YTG | CTT | CAC | AAA | AAC | 389 |
| His      | Ser | Asp     | Gln  | Ile     | Met | Thr | Phe | Arg | Glu | Arg | Leu | Leu | His | Lys | Asn |     |
|          |     |         |      | 90      |     |     |     | 95  |     |     |     |     |     | 100 |     |     |
| TTG      | CAG | GAG     | CAT  | TTT     | TCA | AAC | CAA | GAC | CTT | GTT | TTT | CTG | CTA | TTA | ACA | 437 |
| Leu      | Gln | Glu     | His  | Phe     | Ser | Asn | Gln | Asp | Leu | Val | Phe | Leu | Leu | Leu | Thr |     |
|          |     |         | 105  |         |     |     |     | 110 |     |     |     |     | 115 |     |     |     |
| CCA      |     |         |      |         |     |     |     |     |     |     |     |     |     |     |     | 440 |
| Pro      |     |         |      |         |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 45..258  
id H81225  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..39
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..38  
id H81225  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..216  
id AA044118  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..225  
id W01412  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 13..226  
id W42797  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 95..230  
id R39635  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..124  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 15..94  
id R39635  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 106..201  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.8  
seq VPMLLLIVGGSFG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```
AAAGTGAGTT AAGGACGTAC TCGTCTTGGT GAGAGCGTGA STGCTGAGAT TTGGGAGTCT 60
GCGCTAGGCC CGCTTGGAGT TCTGAGCCGA TGGAAGAGTT CACTC ATG TTT GCA CCC 117
 Met Phe Ala Pro
 -30

GCG GTG ATG CGT GCT TTT CGC AAG AAC AAG ACT CTC GGC TAT GGA GTC 165
Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val
-25 -20 -15

CCC ATG TTG TTG CTG ATT GTT GGA GGT TCT TTT GGT CTT CGT GAG TTT 213
Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe
-10 -5 1

TCT CAA ATC CGA TAT GAT GCT GTG AAG AGT AAA ATG GAT CCT GAG CGG 261
Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Arg
5 10 15 20
```

## (2) INFORMATION FOR SEQ ID NO: 135:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 440 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 143..345  
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 113..315  
id AA143062  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 335..442  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 304..411  
id AA143062  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..149  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 43..120  
id AA143062  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..345  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 44..317  
id HUM172D06B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 372..442  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 340..410  
id HUM172D06B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 35..73  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 8..46  
id HUM172D06B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 153..442  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 125..414  
id N47594  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 77..147  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 49..119  
id N47594  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..412  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 45..385  
id HUM159G08B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..73  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..47  
id HUM159G08B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 143..367  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 92..316  
id N34957  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 80..147  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 30..97  
id N34957  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 362..429  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 312..379  
id N34957  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 24..431  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.7  
seq AVALSFLGLGWLGA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:



|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAGAGAAAGT GTCGGTCTCC AAG ATG GCG GCC GCC TGG CSD TCT GGT CCG TCT | 53  |
| Met Ala Ala Ala Trp Xaa Ser Gly Pro Ser                           |     |
| -135 -130                                                         |     |
| GCT CCG GAG GCC GTG ACG GCC AGA CTC GTT GGT GTC CTG TGG TTC GTC   | 101 |
| Ala Pro Glu Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val   |     |
| -125 -120 -115                                                    |     |
| TCA GTC ACT ACA GGA CCC TGG GGG GCT GTT GCC ACC TCC GCC GGG GGC   | 149 |
| Ser Val Thr Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly   |     |
| -110 -105 -100 -95                                                |     |
| GAG GAG TCG CTT AAG TGC GAG GAC CTC AAA GTG GGA CAA TAT ATT TGT   | 197 |
| Glu Glu Ser Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys   |     |
| -90 -85 -80                                                       |     |
| AAA GAT CCA AAA ATA AAT GAC GCT ACG CAA GAA CCA GTT AAC TGT ACA   | 245 |
| Lys Asp Pro Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr   |     |
| -75 -70 -65                                                       |     |
| AAC TAC ACA GCT CAT GTT TCC TGT TTT CCA GCA CCC AAC ATA ACT TGT   | 293 |
| Asn Tyr Thr Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys   |     |
| -60 -55 -50                                                       |     |
| AAG GAT TCC AGT GGC AAT GAA ACA CAT TTT ACT GGG AAC GAA GTT GGT   | 341 |
| Lys Asp Ser Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly   |     |
| -45 -40 -35                                                       |     |
| TTT TTC AAG CCC ATA TCT TGC CGA AAT GTA AAT GGC TAT TCC TAC AAA   | 389 |
| Phe Phe Lys Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Lys   |     |
| -30 -25 -20 -15                                                   |     |
| GTG GCA GTC GCA TTG TCT CTT TTT CTT GGA TGG TTG GGA GCA GAT CGA   | 437 |
| Val Ala Val Ala Leu Ser Leu Phe Leu Gly Trp Leu Gly Ala Asp Arg   |     |
| -10 -5 1                                                          |     |
| TTT                                                               | 440 |
| Phe                                                               |     |

## (2) INFORMATION FOR SEQ ID NO: 136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..165
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 136..274  
id HSC1WH101  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 73..211  
id R12437  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 72..210  
id R13448  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 105..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 82..142  
id T69236  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 58..105  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 36..83  
id T69236  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 73..129  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq LLWLALACSPVHT/TL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```
AGTGGCCGTC CGGCCTCNCT GACATGCAGC CCTCTGGACC CCGAGGTTGG ACCCTACTGT 60
GACACACCTA CC ATG CGG ACA CTC TTC AAC CTC CTC TGG CTT GCC CTG GCC 111
 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala
 -15 -10

TGC AGC CCT GTT CAC ACT ACC CTG TCA AAG TCA GAT GCC AAA AAA GCC 159
Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
 -5 1 5 10

ACC TCA GGG 168
```

Thr Ser Gly

## (2) INFORMATION FOR SEQ ID NO: 137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..381  
id C15922  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 224..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 200..328  
id AA100508  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..225
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 96..200  
id AA100508  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..90  
id AA100508  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..353
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 89..421  
id W27023

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 353..394
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 422..463  
id W27023  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 76..245  
id W68781  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 267..361  
id W68781  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..69  
id W68781  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 101..331  
id T80234  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..178
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 62..102  
id T80234  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..37  
id T80234  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 132..257
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
seq ASLFLLLSLTVFS/IV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```
AAGAGGAGAC TGCAGACTTC GGTGAGGAA ACGGGTATTT CATGTCTCAG GGAGTAGGTT 60
TGTGCAGTTA CAGCTTTTCT GTTGGTATGC ATAATTAATA ATTGGAGCTG CAAAGCAGAT 120
CGTGACAAGA G ATG GAC GGT CAG AAG AAA AAT TGG AAG GAC AAG GTT GTT 170
 Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val
 -40 -35 -30

GAC CTC CTG TAC TGG AGA GAC ATT AAG AAG ACT GGA GTG GTG TTT GGT 218
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly
 -25 -20 -15

GCC AGC CTA TTC CTG CTG CTT TCA TTG ACA GTA TTC AGC ATT GTG AGC 266
Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
 -10 -5 1

GTA ACA GCC TAC ATT GCC TTG GCC CTG CTC TCT GTG ACC ATC AGC TTT 314
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe
 5 10 15

AGG ATA TAC AAG GGT GTG ATC CAA GCT ATC CAG AAA TCA GAT GAA GGC 362
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
 20 25 30 35

CAC CCA TTC AGG GCA TAT CTG GAA TCT GAA GTT GCT ATA TCT 404
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser
 40 45
```

## (2) INFORMATION FOR SEQ ID NO: 138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 439..475

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
 region 24..60  
 id AA013254  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 41..94  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.5  
 seq LVLGLVPLILWA/DR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

AACTTTCCCA GTCCTAGGCG GCGGTCAGAT CCTTGCAAGC ATG GTC GCG CCG GGG 55
 Met Val Ala Pro Gly
 -15

CTT GTA CTC GGG CTG GTG CTG CCA TTA ATC CTG TGG GCC GAC AGA AGT 103
Leu Val Leu Gly Leu Val Leu Pro Leu Ile Leu Trp Ala Asp Arg Ser
-10 -5 1

GCA GGT ATT GGT TTT CGC TTT GCT TCA TAC ATC AAT AAT GAT ATG GTG 151
Ala Gly Ile Gly Phe Arg Phe Ala Ser Tyr Ile Asn Asn Asp Met Val
5 10 15

CTG CAG AAG GAG CCT GCT GGG GCA GTG ATA TGG GGC TTC GGT ACA CCT 199
Leu Gln Lys Glu Pro Ala Gly Ala Val Ile Trp Gly Phe Gly Thr Pro
20 25 30 35

GGA GCC ACA GTG ACC GTG ACC CTG CGC CAA GGT CAG GAA ACC ATC ATG 247
Gly Ala Thr Val Thr Val Thr Leu Arg Gln Gly Gln Glu Thr Ile Met
40 45 50

AAG AAA GTG ACC AGT GTG AAA GCT CAC TCT GAT ACG TGG ATG GTG GTA 295
Lys Lys Val Thr Ser Val Lys Ala His Ser Asp Thr Trp Met Val Val
55 60 65

CTG GAT CCT ATG AAG CCT GGA GGR SCT TTC GAA GTG ATG GCA CAA CAG 343
Leu Asp Pro Met Lys Pro Gly Gly Xaa Phe Glu Val Met Ala Gln Gln
70 75 80

ACT TTG GAG AAA ATA AAC TTC ACC CTG AGA GTT CAT GAC GTC CTG TTT 391
Thr Leu Glu Lys Ile Asn Phe Thr Leu Arg Val His Asp Val Leu Phe
85 90 95

GGA GAT GTC TGG CTC TGT AGT GGG CAG AGT AAC ATG CAG ATG ACC GCG 439
Gly Asp Val Trp Leu Cys Ser Gly Gln Ser Asn Met Gln Met Thr Ala
100 105 110 115

CGG GTC TTC AGA TGG CGT CAT GTG KTG GGG CTT TTA 475
Arg Val Phe Arg Trp Arg His Val Xaa Gly Leu Leu
120 125

```

## (2) INFORMATION FOR SEQ ID NO: 139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 82..357  
id AA075901  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..298  
id H25630  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 3..298  
id H43485  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..285  
id H80718  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 28..303  
id AA044211  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 45..107
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5

seq LLTIVGLILPTRG/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

ACCTCTCTCC ACGAGGCTGC CGGCTTAGGA CCCCCAGCTC CGAC ATG TCG CCC TCT 56
 Met Ser Pro Ser
 -20

GGT CGC CTG TGT CTT CTC ACC ATC GTT GGC CTG ATT CTC CCC ACC AGA 104
Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg
-15 -10 -5

GGA CAG ACG TTG AAA GAT ACC ACG TCC AGT TCT TCA GCA GAC TCA ACT 152
Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr
 1 5 10 15

ATC ATG GAC ATT CAG GTC CCG ACA CGA GCC CCA GAT GCA GTC TAC ACA 200
Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr
 20 25 30

GAA CTC CAG CCC ACC TCT CCA ACC CCA ACC TGG CCT GCT GAT GAA ACA 248
Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr
 35 40 45

CCA CAA CCC CAG ACC CAG ACC CAG CAA CTG GAA GGA ACG GAT GGG CCT 296
Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro
 50 55 60

CTA GTG ACA GAT CCA GAG ACA CCA CGG 323
Leu Val Thr Asp Pro Glu Thr Pro Arg
 65 70

```

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 43..330  
id W31335  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..63



(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..42  
id W31335  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 28..352  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 2..326  
id AA094921  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 23..345  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..323  
id AA055130  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 62..183  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 60..181  
id R16450  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 180..245  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 179..244  
id R16450  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..62  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 18..61  
id R16450  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 66..183  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 75..192  
id H94808  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 197..254  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 208..265  
                           id H94808  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 13..153  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.3  
                           seq LALSSLLSLLLFA/GM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

AAGCGCTGAC GC ATG CGC ATA GCT AAC CGC ACC CGG TTC AGC TTG CCT TTC 51
 Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Leu Pro Phe
 -45 -40 -35

TTG GCC AGA GGC GCC GGT TGG ACT CAC GGG CGG GGC ATG ATG GTG GTG 99
Leu Ala Arg Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val
 -30 -25 -20

GGT ACG GGC ACC TCG CTG GCG CTC TCC TCC CTC CTG TCC CTG CTG CTC 147
Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu Leu Leu
 -15 -10 -5

TTT GCT GGG ATG CAG ATG TAC AGC CGT CAG CTG GCC TCC ACC GAG TGG 195
Phe Ala Gly Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp
 1 5 10

CTC ACC ATC CAG GGC GGC CTG CTT GGT TCG GGT CTC TTC GTG TTC TCG 243
Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser
 15 20 25 30

CTC ACT GCC TTC AAT AAT CTG GAG AAT CTT GTC TTT GGC AAA GGA TTC 291
Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe
 35 40 45

CAA GCA AAG ATC TTC CCT GAG ATT CTC CTG TGC CTC CTG TTG GCT CTC 339
Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu
 50 55 60

TTT GCA TCT GGC CCG 354
Phe Ala Ser Gly Pro
 65

```

## (2) INFORMATION FOR SEQ ID NO: 141:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..209  
id R54127  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 221..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 199..295  
id R54127  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 10..303  
id R60167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..205  
id H29628  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 211..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 185..291  
id H29628  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 85..289  
id N40052  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 28..116  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..89  
                           id N40052  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 24..230  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 10..216  
                           id R34889  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 221..279  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 206..264  
                           id R34889  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 62..166  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.3  
                           seq NLLLLHCVSRSHS/QN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

ATCTGTGCTG CTGGCCTGGG GTTGTGGTTG AGGCCGTGTC TCCGCTCCTG TGCCCGGGAA 60
G ATG GTG CTA GGT GGT TGC CCG GTT AGT TAC TTA CTT CTG TGC GGC CAG 109
Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln
-35 -30 -25 -20

GCG GCT TTG CTG CTG GGG AAT TTA CTT CTG CTG CAT TGT GTG TCT CGG 157
Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val Ser Arg
-15 -10 -5

AGC CAC TCG CAA AAT GCG ACC GCT GAG CCT GAG CTC ACA TCC GCT GGC 205
Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly
1 5 10

GCC GCC CAG CCG GAG GGC CCC GGG GGT GCT GCG AGC TGG GAA TAT GGC 253
Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly
15 20 25

GAC CCC CAC TCT CCG GTC ATC CTC TGM TCT TAC CTA CCT GAT GAA TTT 301
Asp Pro His Ser Pro Val Ile Leu Xaa Ser Tyr Leu Pro Asp Glu Phe
30 35 40 45

ATA GAA TGT GAA GAC CGG 319
Ile Glu Cys Glu Asp Arg
50

```

## (2) INFORMATION FOR SEQ ID NO: 142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..234  
id T59284  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 263..319  
id T59284  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 340..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 318..365  
id T59284  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 232..268  
id T59284  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..291  
id W52428  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 361..453  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 298..390  
 id W52428  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 79..237  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.1  
 seq IYALFLLVGVCA/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```

AAGTAAATAA TCTCGGAAAG GCGAGAAAGA AGCTGTCTCC ATCTTGTCTG TATCCGCTGC 60
TCTTGTGACG TTGTGGAG ATG GGG AGC GTC CTG GGG CTG TGC TCC ATG GCG 111
 Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala
 -50 -45
AGC TGG ATA CCA TGT TTG TGT GGA AGT GCC CCG TGT TTG CTA TGC CGA 159
Ser Trp Ile Pro Cys Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg
 -40 -35 -30
TGC TGT CCT AGT GGA AAC AAC TCC ACT GTA ACT AGA TTG ATC TAT GCA 207
Cys Cys Pro Ser Gly Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala
 -25 -20 -15
CTT TTC TTG CTT GTT GGA GTA TGT GTA GCN TGT GTA ATG TTG ATA CCA 255
Leu Phe Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro
 -10 -5 1 5
GGA ATG GAA GAA CAA CTG AAT AAG ATT CCT GGA TTT TGT GAG AAT GAG 303
Gly Met Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu
 10 15 20
AAA GGT GTT GTC CCT TGT AAC ATT TTG GTT GGC TAT AAA GCT GTA TAT 351
Lys Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr
 25 30 35
CGT TTG TGC TTT GGT TTG GCT ATG HTC TAT CTT CTT CTC TCT TTA CTA 399
Arg Leu Cys Phe Gly Leu Ala Met Xaa Tyr Leu Leu Leu Ser Leu Leu
 40 45 50
ATG ATC AAA GTG AAG AGT AGC AGT GAT CCT AGA GCT GCA GTG CAC AAT 447
Met Ile Lys Val Lys Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn
 55 60 65 70
GGA TTT
Gly Phe
255

```

## (2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 495 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Brain
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 61..243  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 41..223  
                            id AA102323  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 236..272  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 217..253  
                            id AA102323  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 314..349  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 91  
                            region 298..333  
                            id AA102323  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 268..300  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 93  
                            region 250..282  
                            id AA102323  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 268..434  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 211..377  
                            id H30432  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 147..218  
    (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 88..159  
id H30432  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 209..271  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 151..213  
id H30432  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 250..434  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 71..255  
id H08060  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 61..113  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 35..87  
id H08060  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 449..478  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 268..297  
id H08060  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 77..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 61..149  
id AA088762  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 201..253  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 185..237  
id AA088762  
est

(ix) FEATURE:

(A) NAME/KEY: other



(B) LOCATION: 19..64  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..46  
id AA088762  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..284  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 236..269  
id AA088762  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 126..252  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 102..228  
id HSCOWG121  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 61..127  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 36..102  
id HSCOWG121  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 31..201  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8  
seq IVRLVAFPCPFASS/QV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AATNGCGAGC | NGAACCCGGC | AGCTGGCGCC | ATG | GTG | CTG | TTG | CAC | GTG | CTG | TTT | 54  |     |     |     |     |     |
|            |            |            | Met | Val | Leu | Leu | His | Val | Leu | Phe |     |     |     |     |     |     |
|            |            |            |     |     |     |     |     |     |     |     | -55 |     |     |     |     |     |
| GAG        | CAC        | GCG        | GTC | GGC | TAC | GCG | CTG | CTG | GCG | CTG | AAG | GAA | GTG | GAG | GAG | 102 |
| Glu        | His        | Ala        | Val | Gly | Tyr | Ala | Leu | Leu | Ala | Leu | Lys | Glu | Val | Glu | Glu |     |
|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     | -45 |
|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     | -40 |
|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     | -35 |
| ATC        | AGT        | CTG        | CTG | CAG | CCG | CAG | GTG | GAG | GAG | TCC | GTG | CTC | AAC | CTG | GGC | 150 |
| Ile        | Ser        | Leu        | Leu | Gln | Pro | Gln | Val | Glu | Glu | Ser | Val | Leu | Asn | Leu | Gly |     |
|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     | -30 |
|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     | -25 |
|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     | -20 |
| AAA        | TTC        | CAC        | AGC | ATC | GTT | CGT | CTG | GTG | GCC | TTT | TGT | CCC | TTT | GCC | TCA | 198 |
| Lys        | Phe        | His        | Ser | Ile | Val | Arg | Leu | Val | Ala | Phe | Cys | Pro | Phe | Ala | Ser |     |
|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     | -15 |
|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     | -10 |
|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     | -5  |
| TCC        | CAG        | GTT        | GCC | TTG | GAA | AAT | GCC | AAC | GCC | GTG | TCT | GAA | GGG | GTT | GTT | 246 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Gln | Val | Ala | Leu | Glu | Asn | Ala | Asn | Ala | Val | Ser | Glu | Gly | Val | Val |     |  |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| CAT | GAG | GAC | CTC | CGC | CTG | CTC | TTG | GAG | ACC | CAC | CTG | CCG | TCC | AAA | AAG | 294 |  |
| His | Glu | Asp | Leu | Arg | Leu | Leu | Leu | Glu | Thr | His | Leu | Pro | Ser | Lys | Lys |     |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| AAG | AAA | GTA | CTC | TTG | GGA | GTT | GGG | GAT | CCC | AAG | ATT | GGT | GCC | GCA | ATA | 342 |  |
| Lys | Lys | Val | Leu | Leu | Gly | Val | Gly | Asp | Pro | Lys | Ile | Gly | Ala | Ala | Ile |     |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| CAG | GAG | GAG | TTA | GGG | TAC | AAC | TGC | CAG | ACT | GGA | GGA | GTC | ATA | GCT | GAG | 390 |  |
| Gln | Glu | Glu | Leu | Gly | Tyr | Asn | Cys | Gln | Thr | Gly | Gly | Val | Ile | Ala | Glu |     |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| ATC | CTG | CGA | RGA | GTT | CGT | CTG | CAC | TTC | CAC | AAT | CTG | GTG | AAA | GGG | TCT | 438 |  |
| Ile | Leu | Arg | Xaa | Val | Arg | Leu | His | Phe | His | Asn | Leu | Val | Lys | Gly | Ser |     |  |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |  |
| GAC | CGA | TGT | GKT | CAG | CTT | GTA | AAG | CAC | AGC | TGG | GGC | TGG | GAC | ACA | GCT | 486 |  |
| Asp | Arg | Cys | Xaa | Gln | Leu | Val | Lys | His | Ser | Trp | Gly | Trp | Asp | Thr | Ala |     |  |
|     |     |     | 80  |     |     |     | 85  |     |     | 90  |     |     |     |     | 95  |     |  |
| ATT | CCC | ATG |     |     |     |     |     |     |     |     |     |     |     |     |     | 495 |  |
| Ile | Pro | Met |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

## (2) INFORMATION FOR SEQ ID NO: 144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 20..263  
id H52756  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..186
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 10..195  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 172..262  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 182..272  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 9..262  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..255  
id R78970  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..186  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..180  
id R64509  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 172..262  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 167..257  
id R64509  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 14..228  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 29..243  
id T73900  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 83..223  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```
GAAGAGGCCG CTCTTCCTGG GGTGTTTCT CCGTGTGACG TGTGGCCTTT GAGATCAACT 60
CTCCTGTACC AGCGTAGGCC GC ATG AGT GGG GGG CGG GCT CCC GCG GTC CTG 112
 Met Ser Gly Gly Arg Ala Pro Ala Val Leu
 -45 -40
CTC GGC GGA GTG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG 160
```

```

Leu Gly Gly Val Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala
 -35 -30 -25

CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG 208
Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu
 -20 -15 -10

ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT 256
Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp
 -5 1 5 10

TCC GGC ATC GGG
Ser Gly Ile Gly
 15

```

268

## (2) INFORMATION FOR SEQ ID NO: 145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..177
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..164  
id T09311  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 54..131
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq LVGFILFLTRSRG/RA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

ATGAGATCCC GGCCTCAGGG TGGACGCAGT GGTTCCTGCAC TGAGGCCCTC GTC ATG 56
 Met

GTG GCG CCT GTG TGG TAC TTG GTA GCG GCG GCT CTG CTA GTC GGC TTT 104
Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe
-25 -20 -15 -10

ATC CTC TTC CTG ACT CGC AGC CGG GGC CGG GCG GCA TCA GCC GGC CAA 152
Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln
 -5 1 5

```

GAG CCA CTG CAC AAT GAG GAG CCG GGG  
Glu Pro Leu His Asn Glu Glu Pro Gly  
10 15

179

## (2) INFORMATION FOR SEQ ID NO: 146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..432
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 300..403  
id AA182502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 70..161  
id AA182502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 185..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 153..246  
id AA182502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..77  
id AA182502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 275..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 244..295  
id AA182502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..88  
id AA088802  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 275..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 240..321  
id AA088802  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 206..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 170..242  
id AA088802  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 348..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 314..378  
id AA088802  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 103..156  
id AA088802  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 37..207  
id W52153  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 323..432

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 259..368  
 id W52153  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 272..326  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 207..261  
 id W52153  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 66..109  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 1..44  
 id W52153  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 38..181  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.6  
 seq FLLVRKLPPLCHG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ACGACGCCGG CGAGCAGTGG CCGTKACGGC CGAAAAG ATG GCG GTC TTG GCA CCT | 55  |
| Met Ala Val Leu Ala Pro                                          |     |
| -45                                                              |     |
| CTA ATT GCT CTC GTG TAT TCG GTG CCG CGA CTT TCA CGA TGG CTC GCC  | 103 |
| Leu Ile Ala Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala  |     |
| -40 -35 -30                                                      |     |
| CAA CCT TAC TAC CTT CTG TCG GCC CTG CTC TCT GCT GCC TTC CTA CTC  | 151 |
| Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu  |     |
| -25 -20 -15                                                      |     |
| GTG AGG AAA CTG CCG CCG CTC TGC CAC GGT CTG CCC ACC CAA MGC GAA  | 199 |
| Val Arg Lys Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Xaa Glu  |     |
| -10 -5 1 5                                                       |     |
| GAC GGT AAC CCG TGT GAC TTT GAC TGG AGA GAA GTG GAG ATC CTG ATG  | 247 |
| Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met  |     |
| 10 15 20                                                         |     |
| TTT CTC AGT GCC ATT GTG ATG ATG AAG AAC CGC AGA TCC ATC ACT GTG  | 295 |
| Phe Leu Ser Ala Ile Val Met Met Lys Asn Arg Arg Ser Ile Thr Val  |     |
| 25 30 35                                                         |     |
| GAG CAA CAT ATA GGC AAC ATT TTC ATG TTT AGT AAA GTG GCC AAC ACA  | 343 |
| Glu Gln His Ile Gly Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr  |     |
| 40 45 50                                                         |     |

ATT CTT TTC TTC CGC TTG GAT ATT CGC ATG GGC CTA CTT TAC ATC ACA 391  
Ile Leu Phe Phe Arg Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr  
55 60 65 70

CTC TGC ATA GTG TTC CTG ATG ACG TGC AAA CCC CCC CTT 430  
Leu Cys Ile Val Phe Leu Met Thr Cys Lys Pro Pro Leu  
75 80

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..88  
id AA088802  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 309..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 240..321  
id AA088802  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 240..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 170..242  
id AA088802  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 382..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 314..378  
id AA088802  
est



## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 175..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 103..156  
id AA088802  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 137..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 37..207  
id W52153  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..453
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 259..355  
id W52153  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 306..360
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 207..261  
id W52153  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..44  
id W52153  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 48..300  
id H15999  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 1..42  
id H15999

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 9..215  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.6  
 seq FLLVRKLPPLCHG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

AAGTCGTT ATG GTG GGG GAG GCG GGG CGA GAC CTA CGA CGC CGG CGA SCW 50
 Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Xaa
 -65 -60

KTG GCC GTT ACG GCC GDD AAG ATG GCG GTC TTG GCA CCT CTA ATT GCT 98
Xaa Ala Val Thr Ala Xaa Lys Met Ala Val Leu Ala Pro Leu Ile Ala
-55 -50 -45 -40

CTC GTG TAT TCG GTG CCG CGA CTT TCA CGA TGG CTC GCC CAA CCT TAC 146
Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
 -35 -30 -25

TAC CTT CTG TCG GCC CTG CTC TCT GCT GCC TTC CTA CTC GTG AGG AAA 194
Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys
 -20 -15 -10

CTG CCG CCG CTC TGC CAC GGT CTG CCC ACC CAA CGC GAA GAC GGT AAC 242
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn
 -5 1 5

CCG TGT GAC TTT GAC TGG AGA GAA GTG GAG ATC CTG ATG TTT CTC AGT 290
Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser
10 15 20 25

GCC ATT GTG ATG ATG AAG AAC CGC AGA TCC ATC ACT GTG GAG CAA CAT 338
Ala Ile Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His
 30 35 40

ATA GCC AAC ATT TTC ATG TTT AGT AAA GTG GCC AAC ACA ATT CTT TTC 386
Ile Ala Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe
 45 50 55

TTC CGC TTG GAT ATT CGC ATG GGC CTA CTT TAC ATC ACA CTC TGC ATA 434
Phe Arg Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile
 60 65 70

GTG TTC CTG ATG ACG TGC
Val Phe Leu Met Thr Cys
 75

```

## (2) INFORMATION FOR SEQ ID NO: 148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 236..362

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 178..304  
id W69812  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 61..184

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..124  
id W69812  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 359..423

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 302..366  
id W69812  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 184..236

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 125..177  
id W69812  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 35..395

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 1..361  
id T09075  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 79..386

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..308  
id W45253  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 386..438  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 309..361  
id W45253  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 18..417  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..400  
id AA105440  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..288  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 9..295  
id H42261  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 21..164  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq LLMLLLFLSELQY/YL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```
ACCCTTTCCG GMMGGTCCCC ATG GAG GCG CTG GGG AAG CTG AAG CAG TTC GAT 53
 Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp
 -45 -40

GCC TAC CCC AAG ACT TTG GAG GAC TTC CGG GTC AAG ACC TGC GGG GGC 101
Ala Tyr Pro Lys Thr Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly
 -35 -30 -25

GCC ACC GTG ACC ATT GTC AGT GGC CTT CTC ATG CTG CTA CTG TTC CTG 149
Ala Thr Val Thr Ile Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu
 -20 -15 -10

TCC GAG CTG CAG TAT TAC CTC ACC ACG GAG GTG CAT CCT GAG CTC TAC 197
Ser Glu Leu Gln Tyr Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr
 -5 1 5 10

GTG GAC AAG TCG CGG GGA GAT AAA CTG AAG ATC AAC ATC GAT GTA CTT 245
Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu
 15 20 25

TTT CCG CAC ATG CCT TGT GCC TAT CTG AGT ATT GAT GCC ATG GAT GTG 293
Phe Pro His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val
 30 35 40
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GCC | GGA | GAA | CAG | CAG | CTG | GAT | GTG | GAA | CAC | AAC | CTG | TTC | AAG | CAA | CGA | 341 |
| Ala | Gly | Glu | Gln | Gln | Leu | Asp | Val | Glu | His | Asn | Leu | Phe | Lys | Gln | Arg |     |
| 45  |     |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     |
| CTA | GAT | AAA | GAT | GGC | ATC | CCC | GTG | AGC | TCA | GAG | GCT | GAG | CGG | CAT | GAG | 389 |
| Leu | Asp | Lys | Asp | Gly | Ile | Pro | Val | Ser | Ser | Glu | Ala | Glu | Arg | His | Glu |     |
| 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| CTT | GGG | AAA | GTC | GAG | GTG | ACG | GTG | TTT | GAC | CCT | GAC | TCC | CTG | GAC | CCG | 437 |
| Leu | Gly | Lys | Val | Glu | Val | Thr | Val | Phe | Asp | Pro | Asp | Ser | Leu | Asp | Pro |     |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     |     | 90  |     |

## (2) INFORMATION FOR SEQ ID NO: 149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 70..161  
id AA182502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 304..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 300..392  
id AA182502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..253
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 153..246  
id AA182502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..84
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..77

id AA182502  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 250..301
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 244..295  
id AA182502  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 37..207  
id W52153  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 298..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 259..357  
id W52153  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 247..301
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 207..261  
id W52153  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..84
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..44  
id W52153  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 409..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 370..406  
id W52153  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..103
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..88  
id AA088802  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 250..331  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 240..321  
id AA088802  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 181..253  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 170..242  
id AA088802  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 323..387  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 314..378  
id AA088802  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 116..169  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 103..156  
id AA088802  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 409..446  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 444..481  
id W57342  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 13..156  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

ACGGCCGAAA AG ATG GCG GTC TTG GCA CCT CTA ATT GCT CTC GTG TAT TCG 51

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser  
-45 -40

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GTG CCG CGA CTT TCA CGA TGG CTC GCC CAA CCT TAC TAC CTT CTG TCG | 99  |
| Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser |     |
| -35 -30 -25 -20                                                 |     |
| GCC CTG CTC TCT GCT GCC TTC CTA CTC GTG AGG AAA CTG CCG CCG CTC | 147 |
| Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu |     |
| -15 -10 -5                                                      |     |
| TGC CAC GGT CTG CCC ACC CAA CGC GAA GAC GGT AAC CNN TGT GAC TTT | 195 |
| Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Xaa Cys Asp Phe |     |
| 1 5 10                                                          |     |
| GAC TGG AGA GAA GTG GAG ATC CTG ATG TTT CTC AGT GCC ATT GTG ATG | 243 |
| Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met |     |
| 15 20 25                                                        |     |
| ATG AAG AAC CGC AGA TCC ATC ACT GTG GAG CAA CAT ATA GGC AAC ATT | 291 |
| Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile |     |
| 30 35 40 45                                                     |     |
| TTC ATG TTT AGT AAA GTG GCC AAC ACA ATT CTT TTC TTC CGC TTG GAT | 339 |
| Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp |     |
| 50 55 60                                                        |     |
| ATT CGC ATG GGC CTA CTT TRC ATC ACA CTC TGC ATA GTG TTC CTG ATG | 387 |
| Ile Arg Met Gly Leu Leu Xaa Ile Thr Leu Cys Ile Val Phe Leu Met |     |
| 65 70 75                                                        |     |
| ACG TGC AAA CCC CCC CTA TAT ATG GGC CCT GAG TAT ATC AVG TAC TTC | 435 |
| Thr Cys Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa Tyr Phe |     |
| 80 85 90                                                        |     |
| AAT GAT AAA                                                     | 444 |
| Asn Asp Lys                                                     |     |
| 95                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..272



id C18312  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 281..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 259..385  
id C18312  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 87..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 59..265  
id R99140  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 281..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 252..339  
id R99140  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 22..68  
id R99140  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 92..252  
id T78951  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 281..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 239..314  
id T78951  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..94
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 25..55  
id T78951  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 102..132  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 62..92  
id T78951  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 133..294  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 144..305  
id W69247  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 280..332  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 292..344  
id W69247  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 49..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 62..108  
id W69247  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 97..308  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 69..280  
id H75891  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..69  
id H75891  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 306..335  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 280..309  
 id H75891  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 55..111  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.4  
 seq PMLLRALAQAARA/GP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

AGCCTCCCGA TTGACTGGCC TGCTTGCAA BGCAAGTAGC GCGGCGCTT CAAG ATG 57
 Met

CGC TGC CTG ACC ACG CCT ATG CTG CTG CGG GCC CTG GCC CAG GCT GCA 105
Arg Cys Leu Thr Thr Pro Met Leu Arg Ala Leu Ala Gln Ala Ala
 -15 -10 -5

CGT GCA GGA CCT CCT GGT GGC CGG AGC CTC CAC AGC AGT GCA GTG GCA 153
Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val Ala
 1 5 10

GCC ACC TAC AAG TAT GTG AAC ATG CAG GAT CCC GAG ATG GAC ATG AAG 201
Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met Lys
 15 20 25 30

TCA GTG ACT GAC CGG GCA GCC CGC ACC CTG CTG TGG ACT GAG CTC TTC 249
Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu Phe
 35 40 45

CGA GGC CTG GGC ATG ACC CTG AGC TAC CTG TTC CGG GAA CCG GCC ACC 297
Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Ala Thr
 50 55 60

ATC AAC TAC CCG TTC GAG AAG GGC CCG CTG AGC CCT CGC TTC CGT GGG 345
Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg Gly
 65 70 75

GAG CAT GCG CTG CGC CGG TAC CCA TCC GGG GAG GAG CGT TGC ATT GCC 393
Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile Ala
 80 85 90

TGC AAG CTC TGC
Cys Lys Leu Cys
 95

```

## (2) INFORMATION FOR SEQ ID NO: 151:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE ..  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 2..261

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 13..272  
id C18312  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 249..415

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 259..425  
id C18312  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 55..261

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 59..265  
id R99140  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 17..63

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 22..63  
id R99140  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 101..261

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 92..252  
id T78951  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 249..324

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90  
region 239..314  
id T78951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 62..92  
id T78951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 25..55  
id T78951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..277  
id C16677  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 69..280  
id H75891  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 8..69  
id H75891  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 280..309  
id H75891  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 23..79
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

AAAGTAGCGG CGGCGCTTCA AG ATG CGC TGC CTG ACC ACG CCT ATG CTG CTG 52
 Met Arg Cys Leu Thr Thr Pro Met Leu Leu
 -15 -10

CGG GCC CTG GCC CAG GCT GCA CGT GCA GGA CCT CCT GGT GGC CGG AGC 100
Arg Ala Leu Ala Gln Ala Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser
 -5 1 5

CTC CAC AGC AGT GCA GTG GCA GCC ACC TAC AAG TAT GTG AAC ATG CAG 148
Leu His Ser Ser Ala Val Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln
 10 15 20

GAT CCC GAG ATG GAC ATG AAG TCA GTG ACT GAC CGG GCA GCC CGC ACC 196
Asp Pro Glu Met Asp Met Lys Ser Val Thr Asp Arg Ala Ala Arg Thr
 25 30 35

CTG CTG TGG ACT GAG CTC TTC CGA GGC CTG GGC ATG ACC CTG AGC TAC 244
Leu Leu Trp Thr Glu Leu Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr
 40 45 50 55

CTG TTC CGG GAA CCG NCC ACC ATC AAC TAC CCG TTC GAG AAG GGC CCG 292
Leu Phe Arg Glu Pro Xaa Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro
 60 65 70

CTG AGC CCT CGC TTC CGT GGG GAG CAT GCG CTG CGC CGG TAC CCA TCC 340
Leu Ser Pro Arg Phe Arg Gly Glu His Ala Leu Arg Arg Tyr Pro Ser
 75 80 85

GGG GAG GAG CGT TGC ATT GCC TGC AAG CTC TGC GAG GCC ATC TGC CCC 388
Gly Glu Glu Arg Cys Ile Ala Cys Lys Leu Cys Glu Ala Ile Cys Pro
 90 95 100

GCC CAG GCC ATC ACC ATC GAG GCT GAG 415
Ala Gln Ala Ile Thr Ile Glu Ala Glu
 105 110

```

(2) INFORMATION FOR SEQ ID NO: 152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..349

id N40260  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 351..402  
id N40260  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 22..369  
id W37568  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 14..297  
id AA135041  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 335..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 297..358  
id AA135041  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 74..260  
id W00732  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 302..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 263..347  
id W00732  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..284
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 16..299  
id W07706  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 285..323  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 301..339  
id W07706  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..121  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq ILPLLFGLGVFG/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

GAAGTTGCTT GACTATGGTC TCTCCGGCTA CCAGGAAGAG TCTGCCGAAG TGAAGGCC 58
ATG GAC TTC ATC ACC TCC ACA GCC ATC CTG CCC CTG CTG TTC GGC TGC 106
Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
-20 -15 -10

CTG GGC GTC TTC GGC CTC TTC CGG CTG CTG CAG TGG GTG CGC GGG AAG 154
Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
-5 1 5 10

GCC TAC CTG CGG AAT GCT GTG GTG GTG ATC ACA GGC GCC ACC TCA GGG 202
Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
15 20 25

CTG GGC AAA GAA TGT GCA AAA GTC TTC TAT GCT GCG GGT GCT AAA CTG 250
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
30 35 40

GTG CTC TGT GGC CGG AAT GGT GGG GCC CTA GAA GAG CTC ATC AGA GAA 298
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
45 50 55

CTC ACC GCT TCT CAT GCC ACC AAG GTG CAG ACA CAC AAG CCT TAC TTG 346
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
60 65 70 75

GTA CKN TTN GAC CTC ACA GAC TCT GGG GCC ATA GTT GCA GCA GCA GCT 394
Val Xaa Xaa Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
80 85 90

GAG ATC TGC AGT
Glu Ile Cys Ser
95

```

## (2) INFORMATION FOR SEQ ID NO: 153:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 302 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Lymph ganglia

- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 18..298  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 1..281  
                            id C17369  
                            est

- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 18..298  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 1..281  
                            id HUM522E11B  
                            est

- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 42..298  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 1..257  
                            id HUM503D01B  
                            est

- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 82..298  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 95  
                            region 46..262  
                            id N30487  
                            est

- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 35..70  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 1..36  
                            id N30487  
                            est

- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 19..252

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..234  
id C17067  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 162..248  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq LLLVTWVFTPVT/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```
AGTGTTCGCC GCTGGAGCCC GGGTCGAGAG GACGAGGTGC CGCTGCCTGG AGAATCCTCC 60
GCTGCCGTCTG GCTCCCGGAG CCCAGCCCTT TCCTAACCCA ACCCAACCTA GCCCAGTCCC 120
AGCCGMCAGM GCCTGTCCCT RTCACGGACC CCAGCGTTAC C ATG CAT CCT GCC GTC 176
 Met His Pro Ala Val
 -25

TTC CTA TCC TTA CCC GAC CTC AGA TGC TCC CTT CTG CTC CTG GTA ACT 224
Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu Leu Leu Leu Val Thr
 -20 -15 -10

TGG GTT TTT ACT CCT GTA ACA ACT GAA ATA ACA AGT CTT GAT ACA GAG 272
Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr Ser Leu Asp Thr Glu
 -5 1 5

VGT ATA GAT GAA ATT TTA AAC AAT GCA TTG 302
Xaa Ile Asp Glu Ile Leu Asn Asn Ala Leu
 10 15
```

## (2) INFORMATION FOR SEQ ID NO: 154:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 76..259  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 97.3  
region 1..184  
id HSU72245  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 73..178  
id W25639  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 179..270  
id W25639  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 38..82  
id W25639  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 11..258  
id R72515  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..228  
id AA040016  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..223  
id T84313  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..227
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 129..286  
id H57207

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 225..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 285..319  
id H57207  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 76..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq LVFCVGLLTMAKA/ES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
AAAGTGCTCA GCCCCCGGGG SACAGCAGGA CGTTTGGGGG CCTTCTTTCA GCAGGGGACA 60
GCCCGATTGG GGACA ATG GCG TCT CTT GGC CAC ATC TTG GTT TTC TGT GTG 111
 Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val
 -20 -15 -10

GGT CTC CTC ACC ATG GCC AAG GCA GAA AGT CCA AAG GAA CAC GAC CCG 159
Gly Leu Leu Thr Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro
 -5 1 5

TTC ACT TAC GAC TAC CAG TCC CTG CAG ATC GGA GGC CTC GTC ATC GCC 207
Phe Thr Tyr Asp Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala
 10 15 20

GGG ATC CTC TTC ATC CTG GGC ATC CTC ATC GTG CTG AGC AGA AGA TGC 255
Gly Ile Leu Phe Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys
 25 30 35 40

CGG TTT CGG
Arg Phe Arg 264
```

## (2) INFORMATION FOR SEQ ID NO: 155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..444

(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 91.9  
region 164..604  
id RNGP55  
vrt

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 104..444  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 90.6  
region 567..901  
id RNGP56  
vrt

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 3..444  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 91.4  
region 1..439  
id D50463  
vrt

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 205..298  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 300..393  
id AA173361  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 120..205  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 214..299  
id AA173361  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 1..62  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 95..156  
id AA173361  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 56..119  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 149..212  
id AA173361  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 297..340  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 393..436  
id AA173361  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..339  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..321  
id R14826  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 345..377  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 330..362  
id R14826  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 169..444  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 133..408  
id W75505  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 34..171  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 1..138  
id W75505  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 59..246  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 165..352  
id AA206770  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 284..351  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 393..460  
id AA206770  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 1..69  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
 region 105..173  
 id AA206770  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 243..286  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 351..394  
 id AA206770  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 169..415  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 133..379  
 id W64115  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 34..171  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 1..138  
 id W64115  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 30..98  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.3  
 seq ALSLLLVSGLLP/GP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```

ATTCGCTGTT GGGTCTTCTG CTAGGGAGG ATG TCG GGT TCG TCG CTG CCC AGC 53
 Met Ser Gly Ser Ser Leu Pro Ser
 -20

GCC CTG GCC CTC TCG CTG TTG CTG GTC TCT GGC TCC CTC CTC CCA GGG 101
Ala Leu Ala Leu Ser Leu Leu Leu Val Ser Gly Ser Leu Leu Pro Gly
-15 -10 -5 1

CCA GGC GCC GGT CAG AAC GAG CCA AGG ATT GTC ACC AGT GAA GAG GTC 149
Pro Gly Ala Ala Gln Asn Glu Pro Arg Ile Val Thr Ser Glu Glu Val
 5 10 15

ATT ATT CGA GAC AGC CCT GTT CTC CCT GTC ACC CTG CAG TGT AAC CTC 197
Ile Ile Arg Asp Ser Pro Val Leu Pro Val Thr Leu Gln Cys Asn Leu

```

| 20                                                              | 25  | 30  |     |
|-----------------------------------------------------------------|-----|-----|-----|
| ACC TCC AGC TCT CAC ACC CTT ACA TAC AGC TAC TGG ACA AAG AAT GGG |     |     | 245 |
| Thr Ser Ser Ser His Thr Leu Thr Tyr Ser Tyr Trp Thr Lys Asn Gly |     |     |     |
| 35                                                              | 40  | 45  |     |
| GTG GAA CTG AGT GCC ACT CGT AAG AAT GCC AGC AAC ATG GAG TAC AGG |     |     | 293 |
| Val Glu Leu Ser Ala Thr Arg Lys Asn Ala Ser Asn Met Glu Tyr Arg |     |     |     |
| 50                                                              | 55  | 60  | 65  |
| ATC AAT AAG CCG AGA GCT GAG GAT TCA GGC GAA TAC CAC TGC GTA TAT |     |     | 341 |
| Ile Asn Lys Pro Arg Ala Glu Asp Ser Gly Glu Tyr His Cys Val Tyr |     |     |     |
| 70                                                              | 75  | 80  |     |
| CAC TTT GTC AGC GCT CCT AAA GCA AAC GCC ACC ATT GAA GTG AAA GCC |     |     | 389 |
| His Phe Val Ser Ala Pro Lys Ala Asn Ala Thr Ile Glu Val Lys Ala |     |     |     |
| 85                                                              | 90  | 95  |     |
| GCT CCT GAC ATC ACT GGC CAT AAA CGG AGT DAG AAC AAG AAT GAA GGG |     |     | 437 |
| Ala Pro Asp Ile Thr Gly His Lys Arg Ser Xaa Asn Lys Asn Glu Gly |     |     |     |
| 100                                                             | 105 | 110 |     |
| CAG GAT                                                         |     |     | 443 |
| Gln Asp                                                         |     |     |     |
| 115                                                             |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..130  
id AA056148  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 247..358
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 369..480  
id AA056148  
est

## (ix) FEATURE:



(A) NAME/KEY: other  
(B) LOCATION: 140..251  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 261..372  
id AA056148  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..226  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 227..313  
id AA134519  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 73..143  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 24..94  
id AA134519  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 216..271  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 304..359  
id AA134519  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 294..342  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 384..432  
id AA134519  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..426  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 6..292  
id HUM149F063  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 150..426  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 55..331  
id AA187561  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 140..423  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 77..360  
                           id W51338  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 137..244  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.2  
                           seq IMLLSLAAFSVIS/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```

AGTCTGTCGG ASTCTGTCCT CGGAGCAGGC GGAGTAAAGG GACTTGAGCG AGCCAGTTGC 60
CGGATTATTC TATTTCCCTT CCCTCTCTSC CGCCCCGTAT CTCTTTTCAC CCTTCTCCCA 120
CCCTCGCTCG CGTRSC ATG GCG GTG CAC GAT CTG ATT TTC TGG AGA GAT GTG 172
 Met Ala Val His Asp Leu Ile Phe Trp Arg Asp Val
 -35 -30 -25

AAG AAG ACT GGG TTT GTC TTT GGC ACC ACG CTG ATC ATG CTG CTT TCC 220
Lys Lys Thr Gly Phe Val Phe Gly Thr Thr Leu Ile Met Leu Leu Ser
 -20 -15 -10

CTG GCA GCT TTC AGT GTC ATC AGT GTG GTT TCT TAC CTC ATC CTG GCT 268
Leu Ala Ala Phe Ser Val Ile Ser Val Val Ser Tyr Leu Ile Leu Ala
 -5 1 5

CTT CTC TCT GTC ACC ATC AGC TTC AGG ATC TAC AAG TCC GTC ATC CAA 316
Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val Ile Gln
 10 15 20

GCT GTA CAG AAG TCA GAA GAA GGC CAT CCA TTC AAA GCC TAC CTG GAC 364
Ala Val Gln Lys Ser Glu Glu Gly His Pro Phe Lys Ala Tyr Leu Asp
 25 30 35 40

GTA GAC ATT ACT CTG TCC TCA GAA GCT TTC CAT AAT TAC ATG AAT GCT 412
Val Asp Ile Thr Leu Ser Ser Glu Ala Phe His Asn Tyr Met Asn Ala
 45 50 55

GCS ATG GTG CAC
Ala Met Val His
 60

```

## (2) INFORMATION FOR SEQ ID NO: 157:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 194..260

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 171..237  
id AA213022  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 35..130

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.1  
seq LLWTL LLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```
CTGGCACCTC TTCCGTCGGC TGAATTGCGG CCGT ATG CRC GGC TCT GTG GAG TGC 55
 Met Xaa Gly Ser Val Glu Cys
 -30

ACC TRG GGT TGG GGG CAC TGT GCC CCC AGC CCC CTG CTC CTT TGG ACT 103
Thr Xaa Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr
-25 -20 -15 -10

CTA CTT CTG TTT GCA GCC CCA TTT GGC CTG CTG GGG GAG AAG ACC CGC 151
Leu Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg
 -5 1 5

CAG GTG TCT CTG GAG GTC ATC CCT AAC TGG CTG GGC CCC CTG CAG AAC 199
Gln Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn
 10 15 20

CTG CTT CAT ATA CGG GCA GTG GGC ACC AAT TCC ACA CTG CAC TAT GTG 247
Leu Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val
 25 30 35

TGG AGC AGC CTG GGG CCT CTG GCA GTG GTA ATG GTG GCC ACC AAC ACC 295
Trp Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr
 40 45 50 55

CCC CCC GGG
Pro Pro Gly
304
```

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 47..331

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 30..314  
id AA100852  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 330..429

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 314..413  
id AA100852  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 47..331

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 30..314  
id AA161042  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 338..422

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 323..407  
id AA161042  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 23..335

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 1..313  
id H64488  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..366

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 129..354  
id AA088770  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 32..121  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 17..106  
                           id AA088770  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 116..317  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 134..335  
                           id AA146605  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 317..378  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 336..397  
                           id AA146605  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 137..223  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.1  
                           seq LIFLCGAALLAVG/IW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

```

AAGTGGTGTG TGAGAGCCAG GCGTCCCTCT GCCTGCCCAC TCAGTGGCAA CACCCGGGAG 60
CTGTTTTGTC CTTTGTGGAG CCTCAGCAGT TCCCTCTTTC AGAACTCACT GCCAAGAGCC 120
CTGAACAGGA GCCACC ATG CAG TGC TTC AGC TTC ATT AAG ACC ATG ATG ATC 172
 Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile
 -25 -20

CTC TTC AAT TTG CTC ATC TTT CTG TGT GGT GCA GCC CTG TTG GCA GTG 220
Leu Phe Asn Leu Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val
 -15 -10 -5

GGC ATC TGG GTG TCA ATC GAT GGG GCA TCC TTT CTG AAG ATC TTC GGG 268
Gly Ile Trp Val Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly
 1 5 10 15

CCA CTG TCG TCC AGT GCC ATG CAG TTT GTC AAC GTG GGC TAC TTC CTC 316
Pro Leu Ser Ser Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu
 20 25 30

ATC GCA GCC GGC GTT GTG GTC TTT GCT CTT GGT TTC CTG GGC TGC WMT 364
Ile Ala Ala Gly Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Xaa
 35 40 45

```



|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GCC CCA TTT GGC CTG CTG GGG GAG AAG ACC CAC CAG GTG TCT CTG GAG | 147 |
| Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr His Gln Val Ser Leu Glu |     |
| 1 5 10                                                          |     |
|                                                                 |     |
| GTC ATC CCT AAC TGG CTG GGC CCC CTG CAG AAC CTG CTT CAT ATA CGG | 195 |
| Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg |     |
| 15 20 25                                                        |     |
|                                                                 |     |
| BCA GTG GGC ACC AAT TCC ACA CTG CAC TAT GTG TGG AGC AGC CTG GGG | 243 |
| Xaa Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly |     |
| 30 35 40                                                        |     |
|                                                                 |     |
| CCT CTG GCA GTG GTA ATG GTG GCC ACC AAC ACC CCC CAC AGC ACC CTG | 291 |
| Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu |     |
| 45 50 55 60                                                     |     |
|                                                                 |     |
| AGC GTC AAC TGG AGC CTC CTG CTA TCC CCT GAG CCC GAT GGG GGC CTG | 339 |
| Ser Val Asn Trp Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu |     |
| 65 70 75                                                        |     |
|                                                                 |     |
| ATG GTG CTC CCT AAG GAC AGC ATT CAG TTT TCT TCT                 | 375 |
| Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser                 |     |
| 80 85                                                           |     |

## (2) INFORMATION FOR SEQ ID NO: 160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..234
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 163..233  
id AA113990  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 46..103  
id AA113990  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..44

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 8..50  
id AA113990  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 111..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 113..142  
id AA113990  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 71..202  
id R11825  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 31..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..68  
id R11825  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 112..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 83..205  
id H08475  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..72  
id H08475  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 175..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 142..201  
id C14102  
est

(ix) FEATURE:



(A) NAME/KEY: other  
(B) LOCATION: 60..103  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 25..68  
id C14102  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 136..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..99  
id N87606  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 38..82  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7  
seq LRLKLAATSASA/RV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```
ACCCTTGGGT CCTTGATCCT GAGCTGACCG GGTAGCC ATG GCC TTG CGG CTC CTG 55
 Met Ala Leu Arg Leu Leu
 -15 -10

AAG CTG GCA GCG ACG TCC GCG TCC GCC CGG GTC GTG GCG GCG GGC GCC 103
Lys Leu Ala Ala Thr Ser Ala Ser Ala Arg Val Val Ala Ala Gly Ala
 -5 1 5

CAG CGC GTG AGA GGA ATT CAT AGC AGT GTG CAG TGC AAG CTG CGC TAT 151
Gln Arg Val Arg Gly Ile His Ser Ser Val Gln Cys Lys Leu Arg Tyr
 10 15 20

GGA ATG TGG CAT TTC CTA CTT GGG GAT AAA GCA AGC AAA AGA CTG ACA 199
Gly Met Trp His Phe Leu Leu Gly Asp Lys Ala Ser Lys Arg Leu Thr
 25 30 35

GAA CGC AGC AGA GTG ATA ACT GTA GAT GGC AAT ATG 235
Glu Arg Ser Arg Val Ile Thr Val Asp Gly Asn Met
 40 45 50
```

## (2) INFORMATION FOR SEQ ID NO: 161:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..409  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 55..399  
id AA233701  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..62  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 7..50  
id AA233701  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 148..409  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 106..367  
id N39913  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..151  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..108  
id N39913  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 42..169  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 39..166  
id HUM527C01B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 169..284  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 165..280  
id HUM527C01B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 5..42  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100

region 1..38  
id HUM527C01B  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..118  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 8..107  
id AA280711  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 62..256  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7  
seq IGHFLCLVILVYC/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```
CTCTGTGGAT TCTGGCCAGG CCGGGTTCGG CGGTTGCTGT GAGAGCGGGC TTCCCAACAC 60
C ATG CCG TCC GCC TTC TCT GTC AGC TCT TTC CCC GTC AGC ATC CCA GCC 109
 Met Pro Ser Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
 -65 -60 -55 -50

GTG CTC ACG CAG ACG GAC TGG ACT GAG CCC TGG CTC ATG GGG CTG GCC 157
Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
 -45 -40 -35

ACC TTC CAC GCG CTC TGC GTG CTC CTC ACC TGC TTG TCC TCC CGA AGC 205
Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
 -30 -25 -20

TAC AGA CTA CAG ATC GGG CAC TTT CTG TGT CTA GTC ATC TTA GTC TAC 253
Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
 -15 -10 -5

TGT GCT GAA TAC ATC AAT GAG GCG GCT GCG ATG AAC TGG AGA TTA TTT 301
Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
 1 5 10 15

TCG AAA TAC CAG TAT TTC GAC TCC AGG GGG ATG TTC ATT TCT ATA GTA 349
Ser Lys Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
 20 25 30

TTT TCA GCC CCA CTG CTG GTG AAT GCC ATG ATC ATT GTG GTT ATG TGG 397
Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
 35 40 45

GTA TGG AAG ACT 409
Val Trp Lys Thr
 50
```

## (x) INFORMATION FOR SEQ ID NO: 162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..364
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 192..336  
id T53942  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 59..194  
id T53942  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..58  
id T53942  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 371..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 345..383  
id T53942  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 47..364  
id R55646  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..35
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 18..51  
id R55646  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 32..223  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 47..238  
id H21573  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 220..325  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 236..341  
id H21573  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..35  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 18..51  
id H21573  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..296  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 2..254  
id W47454  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 265..304  
id W47454  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 395..426  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 360..391  
id W47454  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 39..223  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 36..220  
id T71932  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 220..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 218..270  
id T71932  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 4..37  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 2..35  
id T71932  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 26..487  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq ALGILVVAGCSFA/IR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAHCAGACCT CCTCTTGGCT TCGAG ATG GCT TTG CCA CAC CAA GAG CCC AAA | 52  |
| Met Ala Leu Pro His Gln Glu Pro Lys                             |     |
| -150                                                            |     |
| CCT GGA GAC CTG ATT GAG ATT TTC CGC CTT GGC TAT GAG CAC TGG GCC | 100 |
| Pro Gly Asp Leu Ile Glu Ile Phe Arg Leu Gly Tyr Glu His Trp Ala |     |
| -145 -140 -135 -130                                             |     |
| CTG TAT ATA BGA GAT GGC TAC GTG ATC CAT CTG GCT CCT CCA AGT GAG | 148 |
| Leu Tyr Ile Xaa Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu |     |
| -125 -120 -115                                                  |     |
| TAC CCC GGG GCT GGC TCC TCC AGT GTC TTC TCA GTC CTG AGC AAC AGT | 196 |
| Tyr Pro Gly Ala Gly Ser Ser Ser Val Phe Ser Val Leu Ser Asn Ser |     |
| -110 -105 -100                                                  |     |
| GCA GAG GTG AAA CGG GAG CGC CTG GAA GAT GTG GTG GGA GGC TGT TGC | 244 |
| Ala Glu Val Lys Arg Glu Arg Leu Glu Asp Val Val Gly Gly Cys Cys |     |
| -95 -90 -85                                                     |     |
| TAT CGG GTC AAC AAC AGC TTG GAC CAT GAG TAC CAA CCA CGG CCC GTG | 292 |
| Tyr Arg Val Asn Asn Ser Leu Asp His Glu Tyr Gln Pro Arg Pro Val |     |
| -80 -75 -70                                                     |     |
| GAG GTG ATC ATC AGT TCT GCG AAG GAG ATG GTT GGT CAG AAG ATG AAG | 340 |
| Glu Val Ile Ile Ser Ser Ala Lys Glu Met Val Gly Gln Lys Met Lys |     |

| -65                                                             | -60 | -55 | -50 |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| TAC AGT ATT GTG AGC AGG AAC TGT GAG CAC TTT GTC ACC CAG CTG AGA |     |     |     | 388 |
| Tyr Ser Ile Val Ser Arg Asn Cys Glu His Phe Val Thr Gln Leu Arg |     |     |     |     |
|                                                                 | -45 | -40 | -35 |     |
| TAT GGC AAG TCC CGC TGT AAA CAG GTG GAA AAG GCC AAG GTT GAA GTC |     |     |     | 436 |
| Tyr Gly Lys Ser Arg Cys Lys Gln Val Glu Lys Ala Lys Val Glu Val |     |     |     |     |
|                                                                 | -30 | -25 | -20 |     |
| GGT GTG GCC ACG GCG CTT GGA ATC CTG GTT GTT GCT GGA TGC TCT TTT |     |     |     | 484 |
| Gly Val Ala Thr Ala Leu Gly Ile Leu Val Val Ala Gly Cys Ser Phe |     |     |     |     |
|                                                                 | -15 | -10 | -5  |     |
| GCG ATT AGG AGA TAC CAA AAA AAA GCG ACC                         |     |     |     | 514 |
| Ala Ile Arg Arg Tyr Gln Lys Lys Ala Thr                         |     |     |     |     |
| 1                                                               | 5   |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..119  
id AA114211  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 177..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 143..225  
id AA114211  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 30..118  
id AA121286  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 214..287  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 177..250  
id AA121286  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 276..340  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 238..302  
id AA121286  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 35..64  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..30  
id AA121286  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 13..222  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq LAFSLPALPLAEL/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```
AGAGTCGGGA AA ATG GCT GCG AGT ACC TCC ATG GTC CCG GTG GCT GTG ACG 51
 Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr
 -70 -60

GCG GCA GTG GCG CCT GTC CTG TCC ATA AAC AGC GAT TTC TCA GAT TTG 99
Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
 -55 -50 -45

CGG GAA ATT AAA AAG CAA CTG CTG CTT ATT GCG GGC CTT ACC CGG GAG 147
Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu
 -40 -35 -30

CGG GGC CTA CTA CAC AGT AGC AAA TGG TCG GCG GAG TTG GCT TTC TCT 195
Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
 -25 -20 -15 -10

CTC CCT GCA TTG CCT CTG GCC GAG CTG CAA CCG CCT CCG CCT ATT ACA 243
Leu Pro Ala Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr
 -5 1 5

GAG GAA GAT GCC CAG GAT ATG GAT GCC TAT ACC CTG GCC AAG GCC TAC 291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
 10 15 20
```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TTT | GAC | GTT | AAA | GAG | TAT | GAT | CGG | GCA | GCA | CAT | TTC | CTG | CAT | GGC | TGC | 339 |
| Phe | Asp | Val | Lys | Glu | Tyr | Asp | Arg | Ala | Ala | His | Phe | Leu | His | Gly | Cys |     |
| 25  |     |     |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| AAT | GCA | AGA | WAA | GCC | TAT | TTT | CTG | TAT | ATG | TAT | TCC | AGA | TAT | CTG | TCT | 387 |
| Asn | Ala | Arg | Xaa | Ala | Tyr | Phe | Leu | Tyr | Met | Tyr | Ser | Arg | Tyr | Leu | Ser |     |
| 40  |     |     |     |     | 45  |     |     |     | 50  |     |     |     |     | 55  |     |     |

## (2) INFORMATION FOR SEQ ID NO: 164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 116..333  
id H42954  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..117
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..111  
id H42954  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..388
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 332..381  
id H42954  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..436
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 275..404  
id N36051  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..224  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 94..194  
id N36051  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..117  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..89  
id N36051  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 222..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 191..288  
id N36051  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..117  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..111  
id N33866  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 222..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 197..294  
id N33866  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 144..223  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 120..199  
id N33866  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 307..349  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 281..323  
id N33866  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 346..382  
id N33866  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..224
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 65..165  
id N79656  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 162..259  
id N79656  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..117
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..60  
id N79656  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 367..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 307..346  
id N79656  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 86..291  
id HUM424A03B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..117
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..81

id HUM424A03B  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 154..225
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq KMVHLLVLSGAWG/MQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```

AAAACCCACG AGGGGACGCG GCCGAGGAGG GTCGCTGTCC ACCCGGGGGC GTGGGAGTGA 60
GGTACCAGAT TCAGCCCATT TGGCCCCGAC GCCTCTGTTC TCGGAATCCG GGTGCTKGCG 120
GATTNRAGGT CCCGGTTCCT AACGGACTGC AAG ATG GAG GAA GGC GGG AAC CTA 174
 Met Glu Glu Gly Gly Asn Leu
 -20

GGA GGC CTG ATT AAG ATG GTC CAT CTA CTG GTC TTG TCA GGT GCC TGG 222
Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser Gly Ala Trp
 -15 -10 -5

GGC ATG CAA ATG TGG GTG ACC TTC GTC TCA GGC TTC CTG CTT TTC CGA 270
Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg
 1 5 10 15

AGC CTT CCC CGA CAT ACC TTC GGA CTA GTG CAG AGC AAA CTC TTC CCC 318
Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro
 20 25 30

TTC TAC TTC CAC ATC TCC ATG GGC TGT GCC TTC ATC AAY NTC TGC ATC 366
Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Xaa Cys Ile
 35 40 45

TTG GCT TCA CAG CAT GCT TGG GCT CAG CTC ACA TTC TGG GAG GCC AGC 414
Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser
 50 55 60

CAG CTT TAC CTG CTG TTC CTG 435
Gln Leu Tyr Leu Leu Phe Leu
 65 70

```

## (2) INFORMATION FOR SEQ ID NO: 165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..269
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 151..247  
id W04736  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 1..33  
id W04736  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 44..200  
id HUM054D06B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..110
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 6..52  
id HUM054D06B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 6..218  
id HUM065G09B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 44..217  
id HUM062A01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..110
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 5..52

id HUM062A01B  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 66..191  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 10..135  
id HUM048E08B  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 179..276  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 124..221  
id HUM048E08B  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 14..256  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq LLLASGTTLFCTS/FY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATGTTCTACA GCT ATG GCC GGG CCA GCT GCA GCT TTC CGC CGC TTG GGC  | 49  |
| Met Ala Gly Pro Ala Ala Phe Arg Arg Leu Gly                     |     |
| -80 -75 -70                                                     |     |
| GCC TTG TCC GGA GCT GCG GCC TTA GGC TTC GCT TCC TAC GGG GCG CAC | 97  |
| Ala Leu Ser Gly Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His |     |
| -65 -60 -55                                                     |     |
| GGC GCC BAA TTC CCA GAT GCC TAC GGG AAG GAG CTG TTT GAC AAG GCC | 145 |
| Gly Ala Xaa Phe Pro Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala |     |
| -50 -45 -40                                                     |     |
| AAC AAA CAC CAC TTC TTA CAC AGC CTG GCC CTG TTA GGG GTG CCC CAT | 193 |
| Asn Lys His His Phe Leu His Ser Leu Ala Leu Leu Gly Val Pro His |     |
| -35 -30 -25                                                     |     |
| TGC AGA AAG CCA CTC TGG GCT GGG TTA TTG CTA GCT TCC GGA ACG ACC | 241 |
| Cys Arg Lys Pro Leu Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr |     |
| -20 -15 -10                                                     |     |
| TTA TTC TGC ACC AGC TTT TAC TAC CAG GCT CAG                     | 274 |
| Leu Phe Cys Thr Ser Phe Tyr Tyr Gln Ala Gln                     |     |
| -5 1 5                                                          |     |

## (2) INFORMATION FOR SEQ ID NO: 166:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..179
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..143  
id H06750  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..179
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 14..127  
id R09748  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..181
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..76  
id AA025704  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 45..107
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5  
seq LLTLLLPPPPPLYT/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ACTCTTCCGG GTCGGCGCTC CTGCCTCCCT GCAGGGAGCT GCTT ATG GGA CAC CGC | 56  |
| Met Gly His Arg                                                  |     |
| -20                                                              |     |
| TTC CTG CGC GGC CTC TTA ACG CTG CTG CTG CCG CCG CCA CCC CTG TAT  | 104 |
| Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro Pro Pro Leu Tyr  |     |
| -15 -10 -5                                                       |     |
| ACC CGG CAC CGC ATG CTC GGT CCA GAG TCC GTC CCG CCC CCA AAA CGA  | 152 |
| Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro Pro Pro Lys Arg  |     |
| 1 5 10 15                                                        |     |
| TCC CGC AGC AAA CTC ATG GCA CCG CCC CGG                          | 182 |
| Ser Arg Ser Lys Leu Met Ala Pro Pro Arg                          |     |

## (2) INFORMATION FOR SEQ ID NO: 167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 48..320  
id AA081335  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..80
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..49  
id AA081335  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 82..229  
id H88204  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..98  
id H88204  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..160



id W31695  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 111..170
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5  
seq ILFLLPSICSSNS/TG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```
AACATTCACT ASRCCTTTTC CATTGCTAA TAAGGCCCTG CCAGGCTGGG AGGGAATTGT 60
CCCTGCCTGC TTCTGGAGMA MAGAAGATAT TGACACCATC TACGGGCACC ATG GAA 116
 Met Glu
 -20

CTG CTT CAA GTG ACC ATT CTT TTT CTT CTG CCC AGT ATT TGC AGC AGT 164
Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser Ser
-15 -10 -5

AAC AGC ACA GGT GTT TTA GAG GCA GCT AAT AAT TCA CTT GTT GTT ACT 212
Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val Thr
1 5 10

ACA ACA AAW CCA TCT ATA ACA ACA CCA AAC ACA GAA TCA TTA CAG AAA 260
Thr Thr Xaa Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu Gln Lys
15 20 25 30

AAT GTT GTC ACA CCA ACA ACT GGA ACA ACT CHT AAA GGA ACA ATC ACC 308
Asn Val Val Thr Pro Thr Thr Gly Thr Thr Xaa Lys Gly Thr Ile Thr
35 40 45

AAT GAA TTA CTT AAA ATG TCT CTG ATG TCA ACA GCT VCT TTT 350
Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Xaa Phe
50 55 60
```

## (2) INFORMATION FOR SEQ ID NO: 168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 76..372
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 33..329

id H97426  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 369..413  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 327..371  
id H97426  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 23..259  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..238  
id W44834  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 70..120  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 4..54  
id R57989  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 125..154  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 62..91  
id R57989  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 112..168  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```
TTTGACAGTG CCAMAGCTCG GTACTGGACA CAACGAGGGA CCTGGGTCTA CGATAACGCG 60
CTTTTGCTCC TCCTGAAGTG TCTTTGGTCC AACGTTGTTC CAGASTGTAC C ATG GCT 117
 Met Ala

TCC AGT AAC ACT GTG TTG ATG CGG TTG GTA GCC TCC GCA TAT TCT ATT 165
Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr Ser Ile
 -15 -10 -5

GCT CAA AAG GCA GGA ATG ATA GTC AGA CGT GTT ATT GCT GAA GGA GAC 213
Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu Gly Asp
 1 5 10 15
```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CTG GGT ATT GTG GAG AAG ACC TGT GCA ACA GAC CTG CAG ACC AAA GCT | 261 |
| Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr Lys Ala |     |
| 20 25 30                                                        |     |
| GAC CGA TTG GCA CAG ATG AGC ATA TGT TCT TCA TTG GCC CGG AAA TTC | 309 |
| Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg Lys Phe |     |
| 35 40 45                                                        |     |
| CCC AAA CTC ACA ATT ATA GGG GAA GAG GAT CTG CCT TCT GAG GAA GTG | 357 |
| Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu Glu Val |     |
| 50 55 60                                                        |     |
| GAT CAA GAG CTG ATT GAA GAC AGT CAG TGG GAA GAA ATA CTG AAG CAA | 405 |
| Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu Lys Gln |     |
| 65 70 75                                                        |     |
| CCA TGC CCA TCG CAG TAC AGT GCT ATT AAA GAA GAA GAT CTC GTG GTC | 453 |
| Pro Cys Pro Ser Gln Tyr Ser Ala Ile Lys Glu Glu Asp Leu Val Val |     |
| 80 85 90 95                                                     |     |
| TGG GTT GAT                                                     | 462 |
| Trp Val Asp                                                     |     |

## (2) INFORMATION FOR SEQ ID NO: 169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..267  
id HSU46357  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 314..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 291..333  
id HSU46357  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 84..128

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3

seq SSCVLLTALVALA/AY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

GCGGGCAGAA AGTTGCCGGA GGTCTCCGGG TGGTATCGCC CTTTCCTCTT TGCCAGCCCCG 60
CTGGCGAGCC GAGCCGGGGC AAG ATG AGG TCG TCC TGT GTC CTG CTC ACC GCC 113
 Met Arg Ser Ser Cys Val Leu Leu Thr Ala
 -15 -10

CTG GTG GCG CTG GCC GCC TAT TAC GTC TAC ATC CCG CTG CGT GGC TCC 161
Leu Val Ala Leu Ala Ala Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser
 -5 1 5 10

GTG TCC GAC CCC TGG AAG CTG ATG CTG CTG GAC GCC ACT TTC CGG GGT 209
Val Ser Asp Pro Trp Lys Leu Met Leu Leu Asp Ala Thr Phe Arg Gly
 15 20 25

GCA CAG CAA GTG AGT AAC CTG ATC CAC TAC CTG GGA CTG AGC CAT CAC 257
Ala Gln Gln Val Ser Asn Leu Ile His Tyr Leu Gly Leu Ser His His
 30 35 40

CTG CTG GCA CTG AAT TTT ATC ATT GTT TCT TTT GGC AAA AAA AGC GCG 305
Leu Leu Ala Leu Asn Phe Ile Ile Val Ser Phe Gly Lys Lys Ser Ala
 45 50 55

TGG TCT TCT GCC CAA GTG AAG GTG ACC GAC ACA GAC TTT GAT GGT GTG 353
Trp Ser Ser Ala Gln Val Lys Val Thr Asp Thr Asp Phe Asp Gly Val
 60 65 70 75

GAA GTC AGA GTG TTT GAA GGC CCT CCG AAG CCC GAA GAG CCA CTG AAA 401
Glu Val Arg Val Phe Glu Gly Pro Pro Lys Pro Glu Glu Pro Leu Lys
 80 85 90

CGC AGC GTC GTT TAT ATC CAC GGA RGA GGC TGG 434
Arg Ser Val Val Tyr Ile His Gly Xaa Gly Trp
 95 100

```

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..266

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..257  
id H10448  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 9..266  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..258  
id HSC18H071  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..266  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..246  
id AA127134  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..266  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..246  
id HUML13653  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 47..124  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq GVGLVTLLGLAVG/SY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

|                                                                 |            |            |        |             |     |
|-----------------------------------------------------------------|------------|------------|--------|-------------|-----|
| AGGGATCTGT CGGCTTGTC                                            | GGTGGTGGAG | GAAAAGGCGC | TCCGTC | ATG GGG ATC | 55  |
|                                                                 |            |            |        | Met Gly Ile |     |
|                                                                 |            |            |        | -25         |     |
| CAG ACG AGC CCC GTC CTG CTG GCC TCC CTG GGG GTG GGG CTG GTC ACT |            |            |        |             | 103 |
| Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr |            |            |        |             |     |
| -20                                                             | -15        |            |        | -10         |     |
| CTG CTC GGC CTG GCT GTG GGC TCC TAC TTG GTT CGG AGG TCC CGC CGG |            |            |        |             | 151 |
| Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg |            |            |        |             |     |
| -5                                                              | 1          |            | 5      |             |     |
| CCT CAG GTC ACT CTC CTG GAC CCC AAT GAA AAG TAC CTG CTA CGA CTG |            |            |        |             | 199 |
| Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu |            |            |        |             |     |
| 10                                                              | 15         |            | 20     | 25          |     |
| CTA GAC AAG ACG ACT GTG AGC CAC AAC ACC AAG AGG TTC CGC TTT GCC |            |            |        |             | 247 |
| Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala |            |            |        |             |     |

CTG CCC ACC GCC CAC CAC ATG  
Leu Pro Thr Ala His His Met  
45

268

## (2) INFORMATION FOR SEQ ID NO: 171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 53..91  
id N86348  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..40  
id N86348  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 211..241  
id N86348  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..154  
id N88408  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: 52..258  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: \_score 6.3  
 seq ILLIVLFLDAVRE/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

AGCGGRSAGC GCAGGGAGCC AGGCGGGCTG CCGGCGGGTG TGAAGAAAAA A ATG ACA 57
 Met Thr

CTC CAA TGG GCT GCA GTG GCA ACC TTT CTT TAT GCC GAA ATA GGA CTC 105
Leu Gln Trp Ala Ala Val Ala Thr Phe Leu Tyr Ala Glu Ile Gly Leu
 -65 -60 -55

ATT TTA ATC TTC TGC CTA CCT TTT ATT CCT CCT CAG AGA TGG CAG AAG 153
Ile Leu Ile Phe Cys Leu Pro Phe Ile Pro Pro Gln Arg Trp Gln Lys
 -50 -45 -40

ATT TTT TCA TTT AAT GTC TGG GGT AAA ATT GCA ACT TTT TGG AAC AAG 201
Ile Phe Ser Phe Asn Val Trp Gly Lys Ile Ala Thr Phe Trp Asn Lys
 -35 -30 -25 -20

GCT TTC CTT ACC ATT ATC ATC CTA TTG ATT GTT CTA TTT CTA GAT GCT 249
Ala Phe Leu Thr Ile Ile Ile Leu Leu Ile Val Leu Phe Leu Asp Ala
 -15 -10 -5

GTG AGA GAA GTA AGG AAA TAT TCC TCA GTT CAT ACC ATT GAG AAG AGC 297
Val Arg Glu Val Arg Lys Tyr Ser Ser Val His Thr Ile Glu Lys Ser
 1 5 10

TCC ACC AGC AGA CCA AGG
Ser Thr Ser Arg Pro Arg
 15

```

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..138
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
 region 1..122  
 id HSC3DD031  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 137..188  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 120..171  
id HSC3DD031  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 136..188  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 83..135  
id T75196  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 92..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 38..85  
id T75196  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 89..343  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq FLDFCVYIPLSWG/FC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```
AAGAAGCCTG TGTGGCCTTC CCGGCGGCTG ATTCGAGGGC TTGTTTGGTC AGAAGGGGGG 60
CGTCAGAGAA GCTGCCCCCTT AGCCAACC ATG CCG TCT GAG GGT CGC TGC TGG 112
 Met Pro Ser Glu Gly Arg Cys Trp
 -85 -80

GAG ACC TTG AAG GCC CTA CGC AGT TCC GAC AAA GGT CGC CTT TGC TAC 160
Glu Thr Leu Lys Ala Leu Arg Ser Ser Asp Lys Gly Arg Leu Cys Tyr
 -75 -70 -65

TAC CGC GAC TGG CTG CTG CGG CGC GAG GTG AGC GGT GGC CCC GGA GGA 208
Tyr Arg Asp Trp Leu Leu Arg Arg Glu Val Ser Gly Gly Pro Gly Gly
 -60 -55 -50

CGT AGG CCT TTC CGG CCC CTC GCG ACC GAA ACC TTC TCC CTA GCC GTT 256
Arg Arg Pro Phe Arg Pro Leu Ala Thr Glu Thr Phe Ser Leu Ala Val
 -45 -40 -35 -30

GGC ACG TTC TGC TCC CGG GAA CCC GTG CAG TCT AAC AAC CTG CAT TTA 304
Gly Thr Phe Cys Ser Arg Glu Pro Val Gln Ser Asn Asn Leu His Leu
 -25 -20 -15

TTT CTT GAC TTC TGT GTG TAC ATC CCT CTG TCC TGG GGT TTC TGT CCT 352
Phe Leu Asp Phe Cys Val Tyr Ile Pro Leu Ser Trp Gly Phe Cys Pro
```



-10

-5

1

CTT CAG CCT ATT TTA GCG  
Leu Gln Pro Ile Leu Ala  
5

370

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 207..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 217..302  
id N92143  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 308..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 318..391  
id N92143  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 111..182  
id N92143  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..104
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 52..118  
id N92143  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..41

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 1..30  
id N92143  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 119..293  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 91..265  
id R97442  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..125  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 2..98  
id R97442  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 293..381  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 264..352  
id R97442  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(254..378)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..125  
id R97398  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(146..253)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 125..232  
id R97398  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(97..147)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 232..282  
id R97398  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 119..305
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 90..276  
id T80897  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..97  
id T80897  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..100  
id AA047755  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 119..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 93..143  
id AA047755  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 246..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 219..262  
id AA047755  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 203..245
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 175..217  
id AA047755  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 169..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 142..176  
id AA047755  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 45..116
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq AILGSTWVALTTG/AL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

AATCCGGGCC GCGCGGGGAA GGGGAGACGT GGGGTAGAGT GACC ATG ACG AAA TTA 56
 Met Thr Lys Leu

GCG CAG TGG CTT TGG GGA CTA GCG ATC CTG GGC TCC ACC TGG GTG GCC 104
Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser Thr Trp Val Ala
-20 -15 -10 -5

CTG ACC ACG GGA GCC TTG GGC CTG GAG CTG CCC TTG TCC TGC CAG GAA 152
Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu Ser Cys Gln Glu
 1 5 10

GTC CTG TGG CCA CTG CCC GCC TAC TTG CTG GTG TCC GCC GGC TGC TAT 200
Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser Ala Gly Cys Tyr
 15 20 25

GCC CTG GGC ACT GTG GGC TAT CGT GTG GCC ACT TTT CAT GAC TGC GAG 248
Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe His Asp Cys Glu
 30 35 40

GAC GCC GCA CGC GAG CTG CAG AGC CAG ATA CAG GAG GCC CGA GCC GAC 296
Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu Ala Arg Ala Asp
 45 50 55 60

TTA GCC CGC ANG GGC TGC GCT TCT GAC AGC CTA ASC CCA TTC CTG TGC 344
Leu Ala Arg Xaa Gly Cys Ala Ser Asp Ser Leu Xaa Pro Phe Leu Cys
 65 70 75

GGA CAG CCC TTC CTC CCA TTT CCC ATT AAA GAG CCA GGG 383
Gly Gln Pro Phe Leu Pro Phe Pro Ile Lys Glu Pro Gly
 80 85

```

## (2) INFORMATION FOR SEQ ID NO: 174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..205

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 28..189  
id AA122029  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 15..44  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..30  
id AA122029  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 47..232  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 26..211  
id HUML1833  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 113..240  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..128  
id AA158721  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 112..174  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq FLVSNMLLAAYG/SG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```
AAACAAGGGC AGGTCTGACT GCAAGGCTGG GACTGGGAGG CAGAGCCGCC GCCAAGGGGG 60
CCTCGGTTAA ACACTGGTCG TTCAATCACC TGCAAGACGA AGGAGGCAAG G ATG CTG 117
 Met Leu
 -20
TTG GCC TGG GTA CAA GCA TTC CTC GTC AGC AAC ATG CTC CTA GCA GAA 165
Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu Ala Glu
 -15 -10 -5
GCC TAT GGA TCT GGA GGC TGT TTC TGG GAC AAC GGC CAC CTG TAC CGG 213
Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu Tyr Arg
 1 5 10
GAG GAC CAG ACC TCC CCC GCG CCG GGC CTC CGC TGC CTC AAC TGG CTG 261
Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn Trp Leu
 15 20 25
```

GAC GCA CAG AGC GGG  
Asp Ala Gln Ser Gly  
30

276

## (2) INFORMATION FOR SEQ ID NO: 175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 63..212  
id R85337  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 206..338  
id R85337  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 393..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 401..452  
id R85337  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 30..60  
id R85337  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 26..345  
id T86800  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 373..403  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 354..384  
id T86800  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 46..378  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 49..381  
id H94753  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 65..187  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq SVLVLLLLLAVLYE/GI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

AGACTCGGAG CGAGGAGACC CGAGCGAGCA GACGCGGCCC TGGCGCCCGC CCTGCGCACT 60
CACC ATG GCG ATG CAT TTC ATC TTC TCA GAT ACA GCG GTG CTT CTG TTT 109
Met Ala Met His Phe Ile Phe Ser Asp Thr Ala Val Leu Leu Phe
-40 -35 -30

CAT TTC TGG AGT GTC CAC AGT CCT GCT GGC ATG GCC CTT TCG GTG TTG 157
His Phe Trp Ser Val His Ser Pro Ala Gly Met Ala Leu Ser Val Leu
-25 -20 -15

GTG CTC CTG CTT CTG GCT GTA CTG TAT GAA GGC ATC AAG GTT GGC AAA 205
Val Leu Leu Leu Leu Ala Val Leu Tyr Glu Gly Ile Lys Val Gly Lys
-10 -5 1 5

GCC AAG CTG CTC AAC CAG GTA CTG GTG AAC CTG CCA ACC TCC ATC AGC 253
Ala Lys Leu Leu Asn Gln Val Leu Val Asn Leu Pro Thr Ser Ile Ser
10 15 20

CAG CAG ACC ATC GCA GAG ACA GAC GGG GAC TCT GCA GGC TCA GAT TCA 301
Gln Gln Thr Ile Ala Glu Thr Asp Gly Asp Ser Ala Gly Ser Asp Ser
25 30 35

TTC CCT GTT GGC AGA ACC CAC CAC AGG TGG TAT TTG TGT CAC TTT GGC 349
Phe Pro Val Gly Arg Thr His His Arg Trp Tyr Leu Cys His Phe Gly
40 45 50

CAG TCT CTA ATC CAT GTC ATC CAG GTG GTC ATC GGC TAC TTC ATC ATG 397
Gln Ser Leu Ile His Val Ile Gln Val Val Ile Gly Tyr Phe Ile Met
55 60 65 70

```

CTG GCC GTA ATG TCC TAC AAC ACC TGG ATT TTC CTT GGT GTG GTC  
Leu Ala Val Met Ser Tyr Asn Thr Trp Ile Phe Leu Gly Val Val  
75 80 85

442

## (2) INFORMATION FOR SEQ ID NO: 176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 183..278  
id T97803  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 5..84  
id N89398  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(300..345)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 273..318  
id T97702  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 163..387
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq VVXXSVLXTTCXS/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGGGGCAGCG CGGCGTCGCC ATGGCTGAGC TGCAGCAGCT CCGGGTGCAG GAGGCGGTGG 60  
AGTCCATGGT GAAAGTCTG GAAAGAGAGA ACATCCGGAA GATGCAGGGT CTCATGTTCC 120



```

GGTGCAGCGS CAGCYTGTTK GTVAAAGRMC AGCMAGGCCT CC ATG AAG CAG GTG 174
 Met Lys Gln Val
 -75

CAC CAG TGC ATC GAG CGC TGC CAT GTG CCT CTG GCT CAA GCC CAG GCT 222
His Gln Cys Ile Glu Arg Cys His Val Pro Leu Ala Gln Ala Gln Ala
-70 -65 -60

TTG GTC ACC AGT GAG CTG GAG AAG TTC CAG GAC CGC CTG GCC CGG TGC 270
Leu Val Thr Ser Glu Leu Glu Lys Phe Gln Asp Arg Leu Ala Arg Cys
-55 -50 -45 -40

ACC ATG CAT TGC AAC GAC AAA GCC AAA GAT TCA ATA GAT GCT GGG WGT 318
Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser Ile Asp Ala Gly Xaa
-35 -30 -25

AAG GAG CTT CAG GTG AAG CAG CAG CTG AMA GTT GTG TKR MCA AGT GTG 366
Lys Glu Leu Gln Val Lys Gln Gln Leu Xaa Val Val Xaa Xaa Ser Val
-20 -15 -10

TTG RTG ACC ACA TGC AMC TCA TCC CAA CTA 396
Leu Xaa Thr Thr Cys Xaa Ser Ser Gln Leu
-5 1

```

## (2) INFORMATION FOR SEQ ID NO: 177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 10..179  
id AA058587  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..161  
id R20025  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 38..125  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..89  
id R12128  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..193  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 87..156  
id R12128  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 40..193  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 2..155  
id H19999  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 78..193  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..116  
id H83838  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 76..156  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq LLAALMLVAMLQL/LY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```
AAAATCCGGG CTTGCGGCCG CTGGCGTAGT CTGTGGCCGG GTGGTCGTTG CTGCGCGCCC 60
CGAGCCCCGA GAGCC ATG CAG ATG TCC TAC GCC ATC CGG TGC GCC TTC TAC 111
 Met Gln Met Ser Tyr Ala Ile Arg Cys Ala Phe Tyr
 -25 -20

CAG CTG CTG CTG GCC GCG CTC ATG CTG GTG GCG ATG CTG CAG CTG CTC 159
Gln Leu Leu Leu Ala Ala Leu Met Leu Val Ala Met Leu Gln Leu Leu
-15 -10 -5 1

TAC CTG TCG CTG CTG TCC GGA CTA CAC GGG CCG 192
Tyr Leu Ser Leu Leu Ser Gly Leu His Gly Pro
 5 10
```

## (2) INFORMATION FOR SEQ ID NO: 178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..324  
id AA143123  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(192..316)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 312..436  
id AA142922  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(310..376)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 253..319  
id AA142922  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(142..191)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 436..485  
id AA142922  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(130..327)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 7..204  
id H54590  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..376

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 10..145  
id AA013161  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 241..376  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 10..145  
id AA018245  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 198..254  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.1  
seq IILLIHTMQVCTT/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```
AAGTAGCAGA GGCAGCTTCT GAGAGCCTGG GCAGGCAGCA GCTGGCTGAC CAAGTCCACT 60
GGAAGAGAAG GCTTGTGCCA GCCGGGAGAA GGAAGCCGGG GACAGGATGR RAGCAACAAC 120
ACCTTTGCAG ACASTCGACC GGCCCAAGGA CTGGTACAAG ACGATGTTTA AGCAAATTCA 180
CATGGTGCAC AAGCCGG ATG ATG ACA CAG ACA TGT ATA ATA CTC CTT ATA 230
 Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile
 -15 -10

CAT ACA ATG CAG GTC TGT ACA ACC CAC CCT ACA GTG CTC AGT CAC ACC 278
His Thr Met Gln Val Cys Thr Thr His Pro Thr Val Leu Ser His Thr
 -5 1 5

CTG CTG CAA AGA CCC AAA CCT ACA GAC CTC TTT CCA AAA GCC ACT CCG 326
Leu Leu Gln Arg Pro Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro
 10 15 20

ACA ACA GCC CCA ATG CCT TTA AGG ATG CGT CCT CCC CAG TGC CTC CCC 374
Thr Thr Ala Pro Met Pro Leu Arg Met Arg Pro Pro Gln Cys Leu Pro
 25 30 35 40

GAG
Glu 377
```

## (2) INFORMATION FOR SEQ ID NO: 179:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 488 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 109..425  
id AA037143  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..110  
id AA037143  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 443..483
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 423..463  
id AA037143  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..294
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 121..287  
id W37233  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..482
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 367..479  
id W37233  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 293..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 287..324  
id W37233  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 22..57  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 15..50  
id W37233  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 95..128  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 89..122  
id W37233  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 67..96  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 60..89  
id W37233  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 128..424  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 100..396  
id N78012  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 61..128  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 34..101  
id N78012  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 417..464  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 390..437  
id N78012  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..60  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..32  
id N78012  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 107..309  
id W52332  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 353..482
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 335..464  
id W52332  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..108  
id W52332  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 116..305  
id AA081257  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 28..96  
id AA081257  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 95..135  
id AA081257  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 432..467
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 406..441

id AA081257  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 372..437
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq LFLTCLFWPLAAL/NV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```
AGACACTTCC TGGTGGGATC CGAGTGAGGC GACGGGGTAG GGGTTGGCGC TCAGGCGGCG 60
ACCATGGCGT ATCACGGCCT CACTGTGCCT CTCATTGTGA TGAGCGTGTT CTGGGGCTTC 120
GTCGGCTTTC TTGGTGCCTT GGTTCATCCC TAAGGGTCCT AACCGGGGAG TTATCATTAC 180
CATGTTGGTG ACCTGTTTAC TTTGCTGCTA TCTCTTTTGG CTGATTGCAA TTCTGGCCCA 240
ACTCAACCCT CTCTTTGGAC CGCAATTGAA AAATGAAACC ATCTGGTATC TGAAGTATCA 300
TTGGCCTTGA GGAAGAAGAC ATGCTCTACA GTGCTCAGTC TTTGAGGTCA CGAGAAGAGA 360
ATGCCTTCTA G ATG CRN DAT CAC CTC CAA ACC AGA CCA CTT TTC TTG ACT 410
 Met Xaa Xaa His Leu Gln Thr Arg Pro Leu Phe Leu Thr
 -20 -15 -10

TGC CTG TTT TGG CCA TTA GCT GCC TTA AAC GTT AAC AGC ACA TTT GAA 458
Cys Leu Phe Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu
 -5 1 5

TGC CTT ATT CTA CAA TGC AGC GTG GGG ATC 488
Cys Leu Ile Leu Gln Cys Ser Val Gly Ile
 10 15
```

## (2) INFORMATION FOR SEQ ID NO: 180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 139..237  
id T53688  
est



## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..175  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 74..146  
id T53688  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 179..334  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.1  
seq LMAFLLSFYLIPT/NE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

AATGCGCAGA AACACTGGGC ACAGGGGGAG GTAAGTCCCGC TTGGCCCTGG 60  
AGTCCACGCG GATTTTCGAA GCTGGGGCTG GCAAGAGGCC GCTGGACACC ACGCTCCAGT 120  
CGTCAGCCCA CTTCTAGCT GAACAGCGCG AGGCGGCGGC AGCGAGCCGG GTCCCACC 178  
ATG GCC GCG AAT TAT TCC AGT ACC ART ACC CGG AGA GAA CAT GTC AAA 226  
Met Ala Ala Asn Tyr Ser Ser Thr Xaa Thr Arg Arg Glu His Val Lys  
-50 -45 -40  
GTT AAA ACC AGC TCC CAG CCA GGC TTC CTG GAA CGG CTG AGC GAG ACC 274  
Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr  
-35 -30 -25  
TCG GGT GGG ATG TTT GTG GGG CTC ATG GCC TTC CTG CTC TCC TTC TAC 322  
Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr  
-20 -15 -10 -5  
CTA ATT TTC ACC AAT GAG GGC CGC GCA TTG AAG ACG GCA ACC TCA TTG 370  
Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu  
1 5 10  
GCT GAG GGG CTC TCG CTT GTN GTG TCT CCC GAC AGC ATC CAC AGT GTG 418  
Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val  
15 20 25  
GCT CCG GAG AAT GAA GGA ANG CTG GTG CAC ATC ATT 454  
Ala Pro Glu Asn Glu Gly Xaa Leu Val His Ile Ile  
30 35 40

## (2) INFORMATION FOR SEQ ID NO: 181:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 15..215  
id W04921  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 247..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 227..309  
id W04921  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(60..284)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 216..440  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(287..329)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 172..214  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 83..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..139  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 264..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 183..248  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 84..214  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..131  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 247..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 165..247  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 253..315  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.1  
seq LEMLTAFASHIRA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```
AACGAGTTCT TCCGGGGCGG AGGTCACCAT GGCAGCTGCC TTGGCTCGGC TTGGTCTGCG 60
GCCTGTCAAA CAGGTTCTGGG TTCAGTTCTG TCCCTTCGAG AAAAACGTGG AATCGACGAG 120
GACCTTCCTG CAGACGGTGA GCAGTGAGAA GGTCCGCTCC ACTAATCTCA ACTGCTCAGT 180
GATTGCGGAC GTGAGGCATG ACGGCTCCGA GCCCTGCGTG GACGTGCTGT TCGGAACGGG 240
CATCGCCTGA TT ATG CGC GGC GCT CAT CTC ACC GCT CTG GAA ATG CTC ACC 291
 Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Thr
 -20 -15 -10

GCC TTC GCC TCC CAC ATC CGG GCC AGG GAC GCA TCG GGG 330
Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ser Gly
 -5 1 5
```

## (2) INFORMATION FOR SEQ ID NO: 182:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 228..367

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 143..282  
id AA143123  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 89..206  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..118  
id AA143123  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(228..360)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 7..139  
id H54590  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(166..206)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 164..204  
id H54590  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(201..349)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 312..460  
id AA142922  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 274..367  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 10..103  
id AA013161  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 274..367  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 10..103  
id AA018245  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 216..287  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.1  
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

```
AAGTGTATCT GGGCAGCCCC TTCCGGCAAA ACGCAGCAGT AGCAGAGGCA GCTTCTGAGA 60
GCCTGGGCAG GCAGCAGCTG GCTGACCAAG TCCACTGGAA GAGAAGGCTT GTGCCAGCCG 120
GGAGAAGGAA GCCGGGGACA GGATGAAAGC AACAACACCT TTGCAGACAG TCGACCGGCC 180
CAAGGACTGG TACAAGACGA TGTTAAGCAA TTCAC ATG GTG CAC AAG CCG ATG 233
 Met Val His Lys Pro Met
 -20

ATG ACA CAG ACA TGT ATA ATA CTC CTT ATA CAT ACA ATG CAG GTC TGT 281
Met Thr Gln Thr Cys Ile Ile Leu Leu Ile His Thr Met Gln Val Cys
-15 -10 -5

ACA ACC CAC CCT ACA GTG CTC AGT CAC ACC CTG CTG CAA AGA CCC AAA 329
Thr Thr His Pro Thr Val Leu Ser His Thr Leu Leu Gln Arg Pro Lys
1 5 10

CCT ACA GAC CTC TTT CCA AAA GCC ACT CCG ACA ACA 365
Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro Thr Thr
15 20 25
```

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 85..197  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 85..197  
id N43024  
est

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 18..85  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92

region 17..84  
id N43024  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 97..189  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 80..172  
id T62095  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 51..96  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 35..80  
id T62095  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 16..50  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..35  
id T62095  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 51..197  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 26..172  
id W42796  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 100..197  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 114..211  
id AA030227  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 100..197  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 51..148  
id AA118270  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 94..177

(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq IGLMFLMLGCALP/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```
GTGTGTCTGGC CGCCGTAGCG CGTCTTGGGT CTCCCGGCTG CCGCTGCTGC CGCCGCCGCC 60
TCGGGTCGTG GAGCCAGGAG CGACGTCACC GCC ATG GCA GGC ATC AAA GCT TTG 114
 Met Ala Gly Ile Lys Ala Leu
 -25

ATT AGT TTG TCC TTT GGA GGA GCA ATC GGA CTG ATG TTT TTG ATG CTT 162
Ile Ser Leu Ser Phe Gly Gly Ala Ile Gly Leu Met Phe Leu Met Leu
-20 -15 -10

GGA TGT GCC CTT CCA ATA TAC AAC AAA TAC TGG CCT ACG 201
Gly Cys Ala Leu Pro Ile Tyr Asn Lys Tyr Trp Pro Thr
-5 1 5
```

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..268  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 119..252  
id W20516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 25..92  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 12..79  
id W20516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 352..391  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 343..382

id W20516  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..433
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 393..425  
id W20516  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 79..108  
id W20516  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 203..471
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 420..688  
id HSZ78368  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..106
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 46..124  
id HSZ78368  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..204
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 151..220  
id HSZ78368  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 132..300  
id R82255  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..106
- (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 91  
region 24..105  
id R82255  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..31  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 2..31  
id R82255  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 205..471  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 55..321  
id H99530  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 203..358  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 391..546  
id AA209097  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 208..270  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq LLFPLTLVRSFWS/DM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```
AAGAGGGGAA CAAGATGGCG GCGCCGAAGG GGAGCCTCTG GGTGAGGACC CAACTGGGGC 60
TCCCGCGGCT GCTGCTGCTG ACCATGGCCT TGGCCGGAGG TTCGGGGACC GCTTCGGCTG 120
AAGCATTTGA CTCGGKCYTG GKKRATACG GCGTCTTGCC ACCGGGCCTG TCAGTTGACC 180
TACCCCTTGC ACACCTACCC TAAGCTT ATG TCC CTG ATG CCA AAA ATG CAC CTA 234
 Met Ser Leu Met Pro Lys Met His Leu
 -20 -15

CTC TTT CCT CTA ACT CTG GTG AGG TCA TTC TGG AGT GAC ATG ATG GAC 282
Leu Phe Pro Leu Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp
 -10 -5 1

TCC GCA CAG AGC TTC ATA ACC TCT TCA TGG ACT TTT TAT CTT CAA GCC 330
Ser Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala
 5 10 15 20

GAT GAC GGR AAA ATA GTT ATA TTC CAG TCT AAG CCA GAA ATC CAG TAC 378
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asp | Gly | Lys | Ile | Val | Ile | Phe | Gln | Ser | Lys | Pro | Glu | Ile | Gln | Tyr |     |
|     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     | 35  |     |     |
| GCA | CCA | CAT | TTG | GAG | CAG | GAG | CCT | ACA | AAT | TTG | AGA | GAA | TCA | TCT | CTA | 426 |
| Ala | Pro | His | Leu | Glu | Gln | Glu | Pro | Thr | Asn | Leu | Arg | Glu | Ser | Ser | Leu |     |
|     |     |     | 40  |     |     |     | 45  |     |     |     |     |     | 50  |     |     |     |
| AGC | AAA | ATG | TCC | TAT | CTG | CAA | ATG | AGA | AAT | TCA | CAA | GCG | CAC | AGG |     | 471 |
| Ser | Lys | Met | Ser | Tyr | Leu | Gln | Met | Arg | Asn | Ser | Gln | Ala | His | Arg |     |     |
|     |     | 55  |     |     |     |     | 60  |     |     |     |     | 65  |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 123..407  
id W52706  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 69..119  
id W52706  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 38..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq SNILLASVGSVLG/AC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

|            |            |            |         |     |     |     |     |     |     |     |
|------------|------------|------------|---------|-----|-----|-----|-----|-----|-----|-----|
| ATTTCCTGGG | CCAAGTTGGG | ACCCGGACGG | CCTCACC | ATG | ATG | AAA | CGG | GCA | GCT |     |
|            |            |            |         | Met | Met | Lys | Arg | Ala | Ala | 55  |
|            |            |            |         |     |     |     |     |     |     | -85 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GCT | GCT | GCA | GTG | GGA | GGA | GCC | CTG | GCA | GTG | GGG | GCT | GTG | CCC | GTG | GTG | 103 |
| Ala | Ala | Ala | Val | Gly | Gly | Ala | Leu | Ala | Val | Gly | Ala | Val | Pro | Val | Val |     |

-80

-75

-70

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTC | AGT | GCC | ATG | GGC | TTC | ACT | GGG | GCA | GGA | ATC | GCC | GCG | TCC | TCC | ATA | 151 |
| Leu | Ser | Ala | Met | Gly | Phe | Thr | Gly | Ala | Gly | Ile | Ala | Ala | Ser | Ser | Ile |     |
| -65 |     |     |     |     | -60 |     |     |     |     | -55 |     |     |     |     | -50 |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GCA | GCC | AAG | ATG | ATG | TCC | GCA | GCA | GCC | ATT | GCC | AAC | GGG | GGT | GGT | GTT | 199 |
| Ala | Ala | Lys | Met | Met | Ser | Ala | Ala | Ala | Ile | Ala | Asn | Gly | Gly | Gly | Val |     |
|     |     |     | -45 |     |     |     |     |     | -40 |     |     |     |     | -35 |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TCT | GCG | GGG | AGC | CTG | GTG | GCT | ACT | CTG | CAG | TCC | GTG | GGG | GCA | GCT | GGA | 247 |
| Ser | Ala | Gly | Ser | Leu | Val | Ala | Thr | Leu | Gln | Ser | Val | Gly | Ala | Ala | Gly |     |
|     |     |     | -30 |     |     |     |     | -25 |     |     |     |     | -20 |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CTC | TCC | ACA | TCA | TCC | AAC | ATC | CTC | CTG | GCC | TCT | GTT | GGG | TCA | GTG | TTG | 295 |
| Leu | Ser | Thr | Ser | Ser | Asn | Ile | Leu | Leu | Ala | Ser | Val | Gly | Ser | Val | Leu |     |
|     |     | -15 |     |     |     |     | -10 |     |     |     |     | -5  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GGG | GCC | TGC | TTG | GGG | AAT | TCA | CCT | TCH | KCT | TCT | CTC | CCA | GCT | GAA | CCC | 343 |
| Gly | Ala | Cys | Leu | Gly | Asn | Ser | Pro | Ser | Xaa | Ser | Leu | Pro | Ala | Glu | Pro |     |
|     | 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAB | GKN | DAA | GAA | GAT | GAG | GCA | AGA | GAA | AAT | GTA | CCG | CCG |     |     |     | 382 |
| Xaa | Xaa | Xaa | Glu | Asp | Glu | Ala | Arg | Glu | Asn | Val | Pro | Pro |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 117..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 102..301  
id H10706  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 6..101  
id H10706  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 117..316  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 74..273  
id AA043571  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 42..114  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..73  
id AA043571  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 117..316  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 99..298  
id W63643  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 34..114  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 18..98  
id W63643  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 117..316  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 38..237  
id AA081648  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 117..265  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 83..236  
id HUMHBC2885  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 28..114  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..87  
id HUMHBC2885  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 220..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq VTIILLSCXFWA/VK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```
AAAGTAGGGC TGGCGTASGG CCGCCATGTT GCAGCAGGAT AGTAATGATG AACTGAAGA 60
TGTTTCACTG TTTGATGCGG AAGAGGAGAC GACTAATAGA CCAAGRWAAG CCRAVDRRTC 120
AGRCGTCCAG TAGCRTCGTT TTTCCACTTA TTCTTTCGAG TCAGTGCAAT SATCGTCTAT 180
CTTCTCTGTG AGTTGSTCAG CAGCAGCTTT ATTACCTGT ATG GTG ACA ATT ATC 234
 Met Val Thr Ile Ile
 -10

TTG TTG TTG TCG TGT GRC TTT TGG GCA GTG AAG AAT GTC ACA KGT AGA 282
Leu Leu Leu Ser Cys Xaa Phe Trp Ala Val Lys Asn Val Thr Xaa Arg
 -5 1 5

SKA ATG GTT GGC CTA CGT TGG TGG AAT CAC ATT 315
Xaa Met Val Gly Leu Arg Trp Trp Asn His Ile
 10 15
```

## (2) INFORMATION FOR SEQ ID NO: 187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 76..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 123..447  
id W52706  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 69..119  
id W52706

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 14..274  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.8  
 seq SNILLASVGSVSG/AC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```

AGACGGCCTC ACC ATG AWR AAA CGG GCA GCT GCT GCT GCA GTG GGA GGA 49
 Met Xaa Lys Arg Ala Ala Ala Ala Ala Val Gly Gly
 -85 -80

GCC CTG GCA GTG GGG GCT GTG CCC GTG GTG CTC AGT GCC ATG GGC TTC 97
Ala Leu Ala Val Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe
-75 -70 -65 -60

ACT GGG GCA GGA ATC GCC GCG TCC TCC ATA GCA GCC AAG ATG ATG TCC 145
Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser
 -55 -50 -45

GCA GCA GCC ATT GCC AAC GGG GGT GGT GTT TCT GCG GGG AGC CTG GTG 193
Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val
 -40 -35 -30

GCT ACT CTG CAG TCC GTG GGG GCA GCT GGA CTC TCC ACA TCA TCC AAC 241
Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn
 -25 -20 -15

ATC CTC CTG GCC TCT GTT GGG TCA GTG TCG GGG GCC TGC TTG GGG AAT 289
Ile Leu Leu Ala Ser Val Gly Ser Val Ser Gly Ala Cys Leu Gly Asn
-10 -5 1 5

TCA CCT TCT TCT TCT CTC CCA GCT GAA CCC GAG GCT AAA GAA GAT GAG 337
Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp Glu
 10 15 20

GCA AGA GAA AAT GTA CCC CAA GGT GAA CCT CCA AAA CCC CCA CTC AAG 385
Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu Lys
 25 30 35

TCA GAG AAA CAT GAG CGG 403
Ser Glu Lys His Glu Arg
 40

```

## (2) INFORMATION FOR SEQ ID NO: 188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 239..342  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 134..237  
id AA218802  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 129..218  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 22..111  
id AA218802  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 86..352  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq DLSLLSLPPGTSP/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```
AGGCGGCATT TCGGCCCGGC GCCAGGGTGG AGAGTTGTGC GCCGGTCCCT GGGCCTGAGC 60
TCCGGCTCCG GCTGGGGCGC CTGCG ATG TCT CAA GAT GGC GGA STG GGC GAA 112
 Met Ser Gln Asp Gly Gly Xaa Gly Glu
 -85
TTA AAG CAC ATG GTG ATG AGT TTC CGG GTG TCT GAG CTC CAG GTG CTT 160
Leu Lys His Met Val Met Ser Phe Arg Val Ser Glu Leu Gln Val Leu
-80 -75 -70 -65
CTT GGC TTN SCT GGC CGG AAC AAG AGT GGA CGG AAG CAC GAG CTC CTG 208
Leu Gly Xaa Xaa Gly Arg Asn Lys Ser Gly Arg Lys His Glu Leu Leu
 -60 -55 -50
GCC AAG GCT CTG CAC CTC CTG AAG TCC AGC TGT GCC CCT AGT GTC CAG 256
Ala Lys Ala Leu His Leu Leu Lys Ser Ser Cys Ala Pro Ser Val Gln
 -45 -40 -35
ATG AAG ATC AAA GAG CTT TAC CGA CGA CGC TTT CCC CGG AAG ACC CTG 304
Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu
 -30 -25 -20
GGG CCC TCT GAT CTC TCC CTT CTC TCT TTG CCC CCT GGC ACC TCT CCT 352
Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro
 -15 -10 -5
GTA GGC TCC CCT GGT CCT CTA GCT CCC ATT CCC CCA ACG STG TTG GCK 400
Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Xaa Leu Ala
 1 5 10 15
```

STG GCA MCC TGC TGG GCC CCA AGC GTG AGG TGG ACA TGC  
Xaa Ala Xaa Cys Trp Ala Pro Ser Val Arg Trp Thr Cys  
20 25.

439

## (2) INFORMATION FOR SEQ ID NO: 189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..301
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 127..268  
id W31492  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..101  
id W31492  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 331..376  
id W31492  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..151
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..134  
id H85714  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91



region 237..297  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 293..343  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 187..237  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 234..343  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 119..228  
id H52756  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..151  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 20..126  
id H52756  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 342..405  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 228..291  
id H52756  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 35..151  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..118  
id R78970  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 234..343  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 111..220  
id R78970  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 342..385

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 220..263  
id R78970  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 33..151  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..119  
id R64509  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 288..343  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 167..222  
id R64509  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 342..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 222..265  
id R64509  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 268..339  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq LLLPRVLLTMASG/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```
AAATCACGTG GCTGCCACCC AGGTAAGAAG AGGCCGCTCT TCCTGGGGTT GTTCTCCGT 60
GTGACGTGTG GCCTTTGAGA TCAACTCTCC TGTACCAGCG TAGGCCGCAT GAGTGGGGGG 120
CGGGCTCCCG CGGTCCTGCT CGGCGGAGTG GTGAGTGACC GGCCCCGCCC CGCCCCTTCC 180
GGTCCTCGAA GCCTCGACCG CTACCCGCAC CCTAAATCCC AGAGGTTGGC CCCCTGAGGT 240
GCCTCTCTGC TCCTGTCTTT TGTTTGG ATG CCG GMG CTG CTG CCT GTG GCC TCM 294
 Met Pro Xaa Leu Leu Pro Val Ala Ser
 -20

CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG ACC ATG GCC TCT GGA AGC 342
Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser
-15 -10 -5 1

CTC CGA CYC AGC VCT CGM CGG CCT CGG ATT CCG GMT CTG GCT ACG TTC 390
Leu Arg Xaa Ser Xaa Arg Arg Pro Arg Ile Pro Xaa Leu Ala Thr Phe
```

CGG GMT CGG TCT CTG  
Arg Xaa Arg Ser Leu  
20

405

## (2) INFORMATION FOR SEQ ID NO: 190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..397
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 54..373  
id T75227  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 10..73  
id T75227  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 4..251  
id HSC3GD011  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 270..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 29..166  
id HSC01E081  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 243..274  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: . identity 96  
                           region 1..32  
                           id HSC01E081  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 337..407  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..71  
                           id T05865  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 42..146  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
                           seq IFSFLDIVTLCRC/AQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```

GTGTGACTTC GGGCTGTGGG CTCGCTCGCG GCTCTTCGGC C ATG GTT TTC TCA AAC 56
 Met Val Phe Ser Asn
 -35

AAT GAT GAA GGC CTT ATT AAC AAA AAG TTA CCC AAA GAA CTT CTG TTA 104
Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro Lys Glu Leu Leu Leu
-30 -25 -20 -15

AGA ATA TTT TCC TTC TTG GAT ATA GTA ACT TTG TGC CGA TGT GCA CAG 152
Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu Cys Arg Cys Ala Gln
 -10 -5 1

ATT TYM AAG GCT TGG AAC ATC TTA GCC CTG GAT GGA AGC AAC TGG CAA 200
Ile Xaa Lys Lys Ala Trp Asn Ile Leu Ala Leu Asp Gly Ser Asn Trp Gln
 5 10 15

AGA ATA GAT CTT TTT AAC TTT CAA ACA GAT GTA GAG GGT CGA GTG GTG 248
Arg Ile Asp Leu Phe Asn Phe Gln Thr Asp Val Glu Gly Arg Val Val
 20 25 30

GAA AAT ATC TCG AAG CGA TGC GGT GGA TTC CTG AGG AAG CTC AGC TTG 296
Glu Asn Ile Ser Lys Arg Cys Gly Gly Phe Leu Arg Lys Leu Ser Leu
 35 40 45 50

CGA GGC TGC ATT GGT GTT GGG GRT TCC TCC TTG RAG ACC TTT GCA CAG 344
Arg Gly Cys Ile Gly Val Gly Xaa Ser Ser Leu Xaa Thr Phe Ala Gln
 55 60 65

AAC TGC CGA AAC ATT GAA CAT TTG AAC CTC AAT GGA TGC ACA AAA ATC 392
Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn Gly Cys Thr Lys Ile
 70 75 80

ACT GRC AGC ACG TGT
Thr Xaa Ser Thr Cys
 85

```

## (2) INFORMATION FOR SEQ ID NO: 191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..224
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..202  
id HSC3GD011  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..224
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 54..175  
id T75227  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 10..73  
id T75227  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 67..171
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq IFSFLDIVTLCRC/AQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```
AAGGACAACG GCGGTCGCMR GCGCCGTGTG ACTTCGGGCT GTGGGCTCGC TCGCGGCTCT 60
TCGGCC ATG GTT TTC TCA AAC AAT GAT GAA GGC CTT ATT AAC AAA AAG 108
 Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys
 -35 -30 -25
TTA CCC AAA GAA CTT CTG TTA AGA ATA TTT TCC TTC TTG GAT ATA GTA 156
```

Leu Pro Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val  
-20 -15 -10

ACT TTG TGC CGA TGT GCA CAG ATT TCC AAG GCT TGG AAC ATC TTA GCC 204  
Thr Leu Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala  
-5 1 5 10

CTG GAT GGA AGC AAC TGG CAG GGG 228  
Leu Asp Gly Ser Asn Trp Gln Gly  
15

## (2) INFORMATION FOR SEQ ID NO: 192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 36..323  
id W44483  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 305..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 317..410  
id W44483  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 398..447
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 411..460  
id W44483  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(181..321)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 233..373  
id AA035386

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(323..447)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 108..232  
id AA035386  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(109..184)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 371..446  
id AA035386  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(10..64)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 494..548  
id AA035386  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(77..112)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 444..479  
id AA035386  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..420
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 12..417  
id H69070  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 416..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 414..444  
id H69070  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..257  
id AA057029  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..447  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 292..434  
id AA057029  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 180..447  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 167..434  
id W32750  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..185  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 7..171  
id W32750  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 18..353  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq SSCILPWLSKTNS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAGAAGGCTG GGCAGCC ATG GCG TCC TAT TTC GAT GAA CAC GAC TGC GAG  | 50  |
| Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu                     |     |
| -110 -105                                                       |     |
| CCG TCG GAC CCT GAG CAG GAG ACG CGA ACC AAC ATG CTG CTG GAG CTC | 98  |
| Pro Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu |     |
| -100 -95 -90                                                    |     |
| GCA AGG TCA CTT TTC AAT AGG ATG GAC TTT GAA GAC TTG GGG TTG GTA | 146 |
| Ala Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val |     |
| -85 -80 -75 -70                                                 |     |
| GTA GAT TGG GAC CAC CAC CTG CCT CCA CCA GCT GCC AAG ACT GTG GTT | 194 |
| Val Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val |     |
| -65 -60 -55                                                     |     |
| GAG AAC CTC CCC AGG ACA GTC ATC AGA GGC TCT CAG GCT GAG CTC AAG | 242 |
| Glu Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys |     |
| -50 -45 -40                                                     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGC | CCC | GTG | TGT | CTT | TTG | GAA | TTT | GAG | GAG | GAG | GAG | ACT | GCC | ATT | GAG | 290 |
| Cys | Pro | Val | Cys | Leu | Leu | Glu | Phe | Glu | Glu | Glu | Glu | Thr | Ala | Ile | Glu |     |
|     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |     |     |     |
| ATG | CCT | TGC | CAT | CAC | CTT | TTC | CAT | TCC | AGC | TGC | ATT | CTG | CCC | TGG | CTA | 338 |
| Met | Pro | Cys | His | His | Leu | Phe | His | Ser | Ser | Cys | Ile | Leu | Pro | Trp | Leu |     |
|     |     | -20 |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |     |
| AGC | AAG | ACA | AAT | TCC | TGT | CCC | TTG | TGC | CGC | TAT | GAG | CTG | CCC | ACT | GAT | 386 |
| Ser | Lys | Thr | Asn | Ser | Cys | Pro | Leu | Cys | Arg | Tyr | Glu | Leu | Pro | Thr | Asp |     |
|     | -5  |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |
| GAC | GAC | ACT | TAT | GAG | GAG | CAC | AGA | CGA | GAT | AAG | GCT | CGA | AAA | CAG | CAG | 434 |
| Asp | Asp | Thr | Tyr | Glu | Glu | His | Arg | Arg | Asp | Lys | Ala | Arg | Lys | Gln | Gln |     |
|     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |
| CAG | CAA | CAC | CGA | CCA | NGG |     |     |     |     |     |     |     |     |     |     | 452 |
| Gln | Gln | His | Arg | Pro | Xaa |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 30  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..422
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 12..404  
id W22200  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..364
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..332  
id R87595  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 96..309  
id AA031849

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 39..123  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 7..91  
id AA031849  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 122..298  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 110..286  
id R88526  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 12..123  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..112  
id R88526  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 122..376  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 49..303  
id T08643  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 74..125  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..53  
id T08643  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 253..297  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LILSLQVCRPATL/DQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

AAAAAGGGG AGGAAATTGA AACTGAGTGG CCCACGATGG GAAGAGGGGA AAGCCCAGGG 60  
GTACAGGAGG CCTCTGGGTG AAGGCAGAGG CTAACATGGG GTTCGGAGCG ACCTTGCCCG 120

TTGGCCTGAC CATCTTTGTG CTGTCTGTG TCACTATCAT CATCTGCTTC ACCTGCTCCT 180  
GCTGCTGCCT TTACAAGACG TGCCGCCGAC CACGTCCGGT TGTCACCACC ACCACATCCA 240  
CCACTGTGGT GC ATG CCC CTT ATC CTC AGC CTC CAA GTG TGC CGC CCA GCT 291  
Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala  
-15 -10 -5  
ACC CTG GAC CAA GCT ACC AGG GCT ACC ACA CCA TGC CGC CTC AGC CAG 339  
Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln  
1 5 10  
GGA TGC CAG CAG CAC CCT ACC CAA TGC AGT ACC CAC CAC CTT ACC CAG 387  
Gly Cys Gln Gln His Pro Thr Gln Cys Ser Thr His His Leu Thr Gln  
15 20 25 30  
CCC AGC CCA TGG GCC CAC CGG SCT ACC ACG AGA CCC TGG CTG GAG GAG 435  
Pro Ser Pro Trp Ala His Arg Xaa Thr Thr Arg Pro Trp Leu Glu Glu  
35 40 45  
CAG CCG CGC CCC GGG 450  
Gln Pro Arg Pro Gly  
50

## (2) INFORMATION FOR SEQ ID NO: 194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrenals

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 85..139  
id AA157672  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 86..140  
id AA157671  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..94

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 10..47  
id HUML116  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 45..263  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LRRLLGCLTLTSL/GR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

```
AATTGCGTAG TTCCGAATAC CCTCGGCCAC ACCTGGCCTT CTCC ATG CTC GGA ATA 56
 Met Leu Gly Ile
 -70

ACT TCC TGC AGC GAC CAA CAG GCT AAA GAG GGG GAA GGT CTG GAG GGA 104
Thr Ser Cys Ser Asp Gln Gln Ala Lys Glu Gly Glu Gly Leu Glu Gly
 -65 -60 -55

TCC AGC ACC GGC TCC TCC TCC GGC AAC CAC GGT GGG AGC GGC GGA GGA 152
Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly
 -50 -45 -40

AAT GGA CAT AAA CCC GGG TGT GAA AAG CCA GGG AAT GAA GCC CGC GGG 200
Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly
 -35 -30 -25

AGC GGG AAT CTG GGA TTC AGA ACT CTG AGA CGT CTC CTG GGA TGT TTA 248
Ser Gly Asn Leu Gly Phe Arg Thr Leu Arg Arg Leu Leu Gly Cys Leu
 -20 -15 -10

ACT TTG ACA CTT TCT GGA AGA ATT 272
Thr Leu Thr Leu Ser Gly Arg Ile
 -5 1
```

## (2) INFORMATION FOR SEQ ID NO: 195:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..187  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91

region 190..271  
id AA103102  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..108  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 143..191  
id AA103102  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 72..122  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq ALKLASWTSMALA/AS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```
AAATCCCCG CTACCGGGTT GCGGCCGGA GCCGGGCGCC GCGGCTCTGC TTCCCTCGGG 60
GATCTGGCGA C ATG GCC AGA AAG GCT CTC AAG CTT GCT TCG TGG ACC AGC 110
 Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser
 -15 -10 -5
ATG GCT CTT GCT GCC TCT GGC ATC TAC TTC TAC AGT AAC AAG TAC TTG 158
Met Ala Leu Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu
 1 5 10
GAC CCT AAT GAC TTT GGC GCT GTC AGG GTG GGC AGA GCA GTT GCT ACG 206
Asp Pro Asn Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr
 15 20 25
ACG GCT GTC ATC AGT KAC GAC TAC CTC ACT TCC CTG AAG AGT GTC CCT 254
Thr Ala Val Ile Ser Xaa Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro
 30 35 40
TAT GGC TCA GAG GAG TAC TTG CAG CTG AGA TCT AAG GTG CAC CTT CGC 302
Tyr Gly Ser Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg
 45 50 55 60
TCT GCC AGG CGT CTC TGT NAR STC TGC TGT GCC AAC CGG GGC 344
Ser Ala Arg Arg Leu Cys Xaa Xaa Cys Cys Ala Asn Arg Gly
 65 70
```

## (2) INFORMATION FOR SEQ ID NO: 196:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 13..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..394  
id AA284513  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..332  
id H99096  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 363..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 355..395  
id H99096  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 13..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..359  
id AA020823  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 17..396  
id N21197  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 11..277  
id AA083141  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 10..57

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6

-seq AALPAWLSLQSR/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

CTCGCAGCC ATG GCG GCC GCC GCG CTC CCA GCA TGG CTG TCT CTG CAG TCG 51
 Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser
 -15 -10 -5

AGG GCA AGG TCT CTG CGT GCA TTC TCC ACT GCC GTC TAC TCG GCC ACT 99
Arg Ala Arg Ser Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr
 1 5 10

CCG GTC CCG ACA CCT AGC CTG CCG GAA AGA ACA CCC GGA AAT GAA AGG 147
Pro Val Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg
 15 20 25 30

CCA CCA AGN AGA AAG GCA CTA CCT CCT AGG ACA GAG AAA ATG GCT GTT 195
Pro Pro Xaa Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val
 35 40 45

GAC CAG GAC TGG CCT AGT GTT TAC CCA GTT GCA GCA CCA TTB AAA CCC 243
Asp Gln Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Xaa Lys Pro
 50 55 60

TCT GCA GTA CCT CTT CCT GTT CGA ATG GGT TAT CCA GTA AAA AAG GGC 291
Ser Ala Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly
 65 70 75

GTG CCC ATG GCA AAG GAG GGA AAT CTA GAA CTT TTA AAG ATT CCC AAT 339
Val Pro Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro Asn
 80 85 90

TTT CTG CAT TTG ACT CCT GTA GCA ATT AAA AAG CAC TGT GNR GCC CTT 387
Phe Leu His Leu Thr Pro Val Ala Ile Lys Lys His Cys Xaa Ala Leu
 95 100 105 110

AAA GAT TTT TGC ACT GAG 405
Lys Asp Phe Cys Thr Glu
 115

```

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 92..455  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: . identity 97  
region 83..446  
id W37917  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 15..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 5..85  
id W37917  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 104..455  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 95..446  
id AA010474  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 12..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..84  
id AA010474  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 104..314  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 79..289  
id W77834  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 368..455  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 345..432  
id W77834  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 32..106  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 6..80  
id W77834  
est



## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 288..349  
id W77834  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 85..374  
id N78175  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 3..74  
id N78175  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 389..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 370..436  
id N78175  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 183..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 158..430  
id AA169869  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..66  
id AA169869  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..190
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 114..164  
id AA169869

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 104..144  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 77..117  
 id AA169869  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 118..312  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.6  
 seq CMLTLXXLSFILA/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

GTAGTGTTAG ACTGAAGATA AAGTAAGTGC TGTTTGGGCT AACAGGATCT CCTCTTGCAG 60
TCTGCAGCCC AGGACGCTGA TTCCAGCAGC GCCTTACCGC GCASCCGAAG ATTCACT 117
ATG GTG AAA ATC GCC TTC AAT ACC CCT ACC GCC GTG CAA AAG GAG GAG 165
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
-65 -60 -55 -50
GCG CGG CAA GAC GTG GAG GCC CTC CTG AGC CGC ACG GTC AGA ACT CAG 213
Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
-45 -40 -35
ATA CTG ACC GGC AAG GAG CTC CGA GTT GCC ACC CAG GAA AAA GAG GGC 261
Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
-30 -25 -20
TCC TCT GGG AGA TGT ATG CTT ACT CTC TTN NVC CTT TCA TTC ATC TTG 309
Ser Ser Gly Arg Cys Met Leu Thr Leu Xaa Xaa Leu Ser Phe Ile Leu
-15 -10 -5
GCA GGA CTT ATT GTT GGT GGA GCC TGC ATT TAC AAG TAC TTC ATG CCC 357
Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
1 5 10 15
AAG AGC ACC ATT TAC CGT GGA NAG ATG TGC TTT TTT GAT TCT GAG GAT 405
Lys Ser Thr Ile Tyr Arg Gly Xaa Met Cys Phe Phe Asp Ser Glu Asp
20 25 30
CCT GCA AAT TCC CTT CGT GGA GGA GAG CCT AAC TTC CTG CCT GTG ACT 453
Pro Ala Asn Ser Leu Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr
35 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 198:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Thyroid
- (ix) FEATURE:
- (A) NAME/KEY: other
  - (B) LOCATION: 11..171
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 93  
region 1..161  
id HUM085F04B  
est
- (ix) FEATURE:
- (A) NAME/KEY: other
  - (B) LOCATION: 9..109
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 98  
region 1..101  
id AA143653  
est
- (ix) FEATURE:
- (A) NAME/KEY: other
  - (B) LOCATION: complement(62..155)
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 95  
region 24..117  
id H17554  
est
- (ix) FEATURE:
- (A) NAME/KEY: other
  - (B) LOCATION: 103..185
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 90  
region 139..221  
id H18908  
est
- (ix) FEATURE:
- (A) NAME/KEY: other
  - (B) LOCATION: 109..185
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 93  
region 133..209  
id H85714  
est
- (ix) FEATURE:
- (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: 11..154
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 5.6  
seq LLLSFVWMPALLP/DG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

AAACCGCGCC ATG ATA GGG TCG GGA TTG.GCT GGC TCT GGA GGC GCA GGT 49
 Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly
 -45 -40

GGT CCT TCT TCT ACT GTC ACA TGG TGC GCG CTG WTT TCT AAT CAC GTG 97
Gly Pro Ser Ser Thr Val Thr Trp Cys Ala Leu Xaa Ser Asn His Val
-35 -30 -25 -20

GCT GCC ACC CAG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG 145
Ala Ala Thr Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala
 -15 -10 -5

CTG CTG CCT GAT GGC CTC CCG CCW TTT GTT GCT ACC CCG ATG 187
Leu Leu Pro Asp Gly Leu Pro Pro Phe Val Ala Thr Pro Met
 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 2..137  
id N40054  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 202..319  
id N40054  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..422
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 316..406  
id N40054  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 134..190  
id N40054  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 167..284  
id N27721  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..102  
id N27721  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 281..364  
id N27721  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 99..155  
id N27721  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..137
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..133  
id W25483  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..296
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 213..292  
id W25483

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 144..201  
id W25483  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..148
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..124  
id C17967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 194..292  
id C17967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 125..182  
id C17967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 307..354  
id C17967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..165  
id T47061  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 177..294  
id T47061  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 329..369  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 288..328  
id T47061  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 313..366  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LXGFLFXVIVLTS/WI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```
AATAACTGAA AGTAGCTAAG GCACCCCAGC CGGAGGAAGT GAGCTCTCCT GGGGCGTGGT 60
TGTTTCGTGAT CCTTGCATCT GTTACTTAGG GTCAAGGCTT GGGTCTTGCC CCGCAGACCC 120
TTGGGACGAC CCGGCCCCAG CGCASTATGA ACCTGGAGCG AGTGTCCAAT GAGGAGAAAT 180
TGAACCTGTG CCGGAAGTAC TACCTGGGGG GGTTTGCTTT CCTGCCTTTT CTCTGGTTGG 240
TCAACATCTT CTGGTTCTTC CGAGAGGCCT TCCTTGTCCT AGCCTACACA GAACAGAGCC 300
AAATCAAAGG CT ATG TCT GGC GCT CAG CTK HTG GGC TTC CTC TTC TGS GTG 351
 Met Ser Gly Ala Gln Leu Xaa Gly Phe Leu Phe Xaa Val
 -15 -10

ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC CGC 399
Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro Arg
-5 1 5 10

TGG GGG TGC CCT TGG GGA CTA CCT CTC CTT CAC ATA CCC CTG GGC ACC 447
Trp Gly Cys Pro Trp Gly Leu Pro Leu Leu His Ile Pro Leu Gly Thr
 15 20 25

CCT GAC AAC TTC TGC ACA TAC 468
Pro Asp Asn Phe Cys Thr Tyr
 30
```

## (2) INFORMATION FOR SEQ ID NO: 200:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Placenta

## (ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 328..432  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 15..119  
id HUMGS01778  
est

## (ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: complement(256..309)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 175..228  
id HSAAAAJHX  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 188..274  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq VVFMTVAASGASS/FA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

ACGGTTCCGG GCGTTACCAT CGTCCGTGCG CACCGCCCGG CGTCCAGGTG AGTCTCCCAT 60
CTGCAGAGAC GCGGACGCGC CGGCCCGCAG TTGGCCTGCG GACGCGGTGG ACGGTTTGGC 120
GCCCCACCAGG CGATCAATAC TTTGGATTTT TAATTTCTAG ATTTGGCAAT TCTTCGCTGA 180
AGTCATC ATG AGC TTT TTC CAA CTC CTG ATG AAA AGG AAG GAA CTC ATT 229
 Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile
 -25 -20

CCC TTG GTG GTG TTC ATG ACT GTG GCG GCG AGT GGA GCC TCA TCT TTC 277
Pro Leu Val Val Phe Met Thr Val Ala Ala Ser Gly Ala Ser Ser Phe
-15 -10 -5 1

GCT GTG TAT TCT CTT TGG AAA ACC GAT GTG ATC CTT GAT CGA AAA AAA 325
Ala Val Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys
 5 10 15

AAT CCA GAA CCT TGG GAA ACT GTG GAC CCT ACT GTA CCT CAA AAG CTT 373
Asn Pro Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu
 20 25 30

ATA ACA ATC AAC CAA CAA TGG AAA CCC ATT GAA GAG TTG CAA AAT GTC 421
Ile Thr Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val
 35 40 45

CAA AGG GTA ACG 433
Gln Arg Val Thr
50

```



## (2) INFORMATION FOR SEQ ID NO: 201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..242)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..215  
id N91097  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 103..147
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LAHSLLLNEEALA/QI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

GCGGGAGGTG GGGCATCCGG GTCTCTTGGT GGCTGCTTCT ACCCCCGGAG CTCAGCTGAT 60
CTTCCCTTCC AGACTACGAG GTGTGAATTT CAAACTTCCG TA ATG GAG TTA GCC 114
 Met Glu Leu Ala
 -15
CAC AGT TTA TTG CTA AAT GAA GAA GCT TTG GCT CAA ATC ACC GAA GCA 162
His Ser Leu Leu Leu Asn Glu Glu Ala Leu Ala Gln Ile Thr Glu Ala
-10 -5 1 5
AAA AGA CCA GTT TTC ATC TTT GAA TGG TTG CGA TTT CTT GAT AAA GTC 210
Lys Arg Pro Val Phe Ile Phe Glu Trp Leu Arg Phe Leu Asp Lys Val
 10 15 20
TTG GTT GCT GCC AAC AAG ACC GAT GTA AAG GAA AAA CAG AAA AAA CTT 258
Leu Val Ala Ala Asn Lys Thr Asp Val Lys Glu Lys Gln Lys Lys Leu
 25 30 35
GTT GAA CAA TTA ACT GGA TTA ATA AGT AGT TCA CCT GGA CCC ACC GGG 306
Val Glu Gln Leu Thr Gly Leu Ile Ser Ser Ser Pro Gly Pro Thr Gly
 40 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 325 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Prostate
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 6..322  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 15..331  
                            id H23844  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 11..322  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 21..332  
                            id H22656  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 12..310  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 8..306  
                            id AA036876  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 22..204  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..183  
                            id W05714  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 205..305  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 183..293  
                            id W05714  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 40..322

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..283  
id R69117  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 56..139  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq LGYLVLSEGAFLA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| CTGAAGCCGG AAGCTACCTA TCTGGTAGGG AGCTCCCCCA GCACCGAAGA CTGCG ATG | 58  |
| Met                                                              |     |
| ACT TCT GCA CTG ACC CAG GGG CTG GAG CGA ATC CCA GAC CAG CTC GGC  | 106 |
| Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu Gly  |     |
| -25 -20 -15                                                      |     |
| TAC CTG GTA CTG AGT GAA GGT GCA GTG CTG GCG TCA TCT GGG GAC CTG  | 154 |
| Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp Leu  |     |
| -10 -5 1 5                                                       |     |
| GAG AAT GAT GAG CAG GCA GCC AGT GCC ATC TCT GAG CTG GTC AGC ACA  | 202 |
| Glu Asn Asp Glu Gln Ala Ala Ser Ala Ile Ser Glu Leu Val Ser Thr  |     |
| 10 15 20                                                         |     |
| GCC TGC GGT TTC CGG CTG CAC CGC GGC ATG AAT GTG CCC TTC AAG CGC  | 250 |
| Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Phe Lys Arg  |     |
| 25 30 35                                                         |     |
| CTG TCT GTG GTC TTT GGA GAA CAC ACA CTG CTG GTG ACG GTG TCA GGA  | 298 |
| Leu Ser Val Val Phe Gly Glu His Thr Leu Leu Val Thr Val Ser Gly  |     |
| 40 45 50                                                         |     |
| CAG AGG GTG TTT GTG GTG AAG AGG GGG                              | 325 |
| Gln Arg Val Phe Val Val Lys Arg Gly                              |     |
| 55 60                                                            |     |

## (2) INFORMATION FOR SEQ ID NO: 203:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..374  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 125..358  
id N47594  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..135  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 49..119  
id N47594  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 388..452  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 374..438  
id N47594  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 131..333  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 113..315  
id AA143062  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..137  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 43..120  
id AA143062  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 323..374  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 304..355  
id AA143062  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 388..433  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 371..416  
id AA143062  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 44..317  
id HUM172D06B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 388..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 370..416  
id HUM172D06B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 8..46  
id HUM172D06B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 45..359  
id HUM159G08B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..47  
id HUM159G08B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 92..316  
id N34957  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 30..97  
id N34957

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 12..104
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LVGVLFVSVTTG/PW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```

AGGTCTCCAA G ATG GCG GCC GCC TGG CCG TCT GGT CCG KCT GCT CCG GAG 50
 Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
 -30 -25 -20

GCC GTG ACG GCC AGA CTC GTT GGT GTC CTG TGG TTC GTC TCA GTC ACT 98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr
 -15 -10 -5

ACA GGA CCC TGG GGG GCT GTT GCC ACC TCC GCC GGG GGC GAG GAG TCG 146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
 1 5 10

CTT AAG TGC GAG GAC CTC AAA GTG GGA CAA TAT ATT TGT AAA GAT CCA 194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
 15 20 25 30

AAA ATA AAT GAC GCT ACG CAA GAA CCA GTT AAC TGT ACA AAC TAC ACA 242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
 35 40 45

GCT CAT GTT TCC TGT TTT CCA GCA CCC AAC ATA ACT TGT AAG GAT NCC 290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Xaa
 50 55 60

AGT GGC AAT GAA ACA CAT TTT ACT GGG AAC GAA GTT GGT TTT TTC AAG 338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
 65 70 75

CCC ATA TCT TGC CGA AAT GTA AAT GGC TAT TCC TAC NNT KAG CAG TNN 386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Xaa Xaa Gln Xaa
 80 85 90

NWT GTC TCT TTT TCT TGG ATG GTT GGG AGC AGA TCG ATT TTA CCT TGG 434
Xaa Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
 95 100 105 110

ATA CCC TGC TTT GGG TTT GTT 455
Ile Pro Cys Phe Gly Phe Val
 115

```

## (2) INFORMATION FOR SEQ ID NO: 204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 170..201

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 157..188  
id AA102919  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 117..155

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5  
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

AAGCAGCTGG ATCTCCGGTA ACTGAGACAT AGGGTATAAC TGTGTGTCGCG GCGGAGGAAG 60

TGAGGACGGC GCCAAGGGCC TTCCGGGCCA GTGTTGGATC CCTGTAGTTT GTGAAG ATG 119  
Met

GTG TTG CTA ACA ATG ATC GCC CGA GTG GCG GAC GGG CTC CCG CTG GCC 167  
Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu Ala  
-10 -5 1

GCC TCG ATG CAG GAG GAC GAA CAG TCT GGC CGG 200  
Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg  
5 10 15

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 121..436

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 57..372

id AA023107  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..436
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 157..399  
id AA102919  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 141..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq MVLLTMIARVADG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```

AACCTCAGCG GGAAGCGGAG ACGCAAGCAG CTKGATCTCC GGTAAGTGAG ACATAGGGTA 60
TAACTGTTGT CGCGGCGGAG GAAGTGAGGA CGGCGCCAAG GGCCTTCCGG GCCAGTGTG 120
GATCCCTGTA GTTTGTGAAG ATG GTG TTG CTA ACA ATG ATC GCC CGA GTG GCG 173
 Met Val Leu Leu Thr Met Ile Ala Arg Val Ala
 -10 -5

GAC GGG CTC CCG CTG GCC GCC TCG ATG CAG GAG GAC GAA CAG TCT GGC 221
Asp Gly Leu Pro Leu Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly
 1 5 10

CGG GAC CTT CAA CAG TAT CAG AGT CAG GCT AAG CAA CTC TTT CGA AAG 269
Arg Asp Leu Gln Gln Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys
 15 20 25 30

TTG AAT GAA CAG TCC CCT ACC AGA TGT ACC TTG GAA GCA GGA GCC ATG 317
Leu Asn Glu Gln Ser Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met
 35 40 45

ACT TTT CAC TAC ATT ATT GAG CAG GGG GTG TGT TAT TTG GTT TTA TGT 365
Thr Phe His Tyr Ile Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys
 50 55 60

GAA GCT GCC TTC CCT AAG AAG TTG GCT TTT GCC TAC CTA GAA GAT TTG 413
Glu Ala Ala Phe Pro Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu
 65 70 75

CAC TCA GAA TTT GAT GAA CAG 434
His Ser Glu Phe Asp Glu Gln
 80 85

```

## (12) INFORMATION FOR SEQ ID NO: 206:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID



- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 86..333  
id AA035208  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 7..81  
id AA035208  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 363..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 349..378  
id AA035208  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 99..288  
id R97144  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 10..94  
id R97144  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 63..353  
id H64963

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 38..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..58  
id H64963  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 102..392  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 32..322  
id W03796  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 102..356  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 86..340  
id N73170  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 3..81  
id N73170  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 117..323  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.4  
seq MMVLSLGIXLASA/SF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```
AAGAAGATGA AGGTAAGTAG AAACCGTTGA TGGGACTGAG AAACCAGAGT TAAAACCTCT 60
TTGGAGCTTC TGAGGACTCA GCTGGAACCA AMCGGGCACA GGTGGAAC ACCATC ATG 119
 Met
ACA TCA CAA CCT GTT CCC AAT GAG ACC ATC ATA GTG CTC CCA TCA AAT 167
Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser Asn
 -65 -60 -55
GTC ATC AAC TTC TCC CAA GCA GAG AAA CCC GAA CCC ACC AAC CAG GGG 215
Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly
 -50 -45 -40
```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAG GAT AGC CTG AAG AAA CAT CTA CAC GCA GAA ATC AAA GTT ATT GGG | 263 |
| Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile Gly |     |
| -35 -30 -25                                                     |     |
| ACT ATC CAG ATC TTG TGT GGC ATG ATG GTA TTG AGC TTG GGG ATC AKT | 311 |
| Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile Xaa |     |
| -20 -15 -10 -5                                                  |     |
| TTG GCA TCT GCT TCC TTC TCT CCA AAT TTT ACC CAA GTG ACT TCT ACA | 359 |
| Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser Thr |     |
| 1 5 10                                                          |     |
| CTG TTG AAC TCT GCT TAC CCA TTC ATA GGA CCC TTT TTT TTT ATC ATC | 407 |
| Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile |     |
| 15 20 25                                                        |     |
| TCT GGC TCT CTA TCA ATC                                         | 425 |
| Ser Gly Ser Leu Ser Ile                                         |     |
| 30                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 3..347  
id W81335  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 369..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 346..383  
id W81335  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 379..403  
id W81335

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..240  
id W03593  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 239..347  
id W03593  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..234  
id AA156841  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 233..389  
id AA156841  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..177  
id W81261  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 162..310  
id W81261  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 325..406  
id W81261  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 41..273  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..233  
id AA151036  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 273..430  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 232..389  
id AA151036  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 38..112  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq AVTSLLSPTPATA/LA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATTTTTTTTTT CGAGACCGGA AGTGAGTGAT CGAAAGC ATG GCG TCG GTG GTG TTG | 55  |
| Met Ala Ser Val Val Leu                                           |     |
| -25 -20                                                           |     |
| GCG CTG AGG ACC CGG ACA GCC GTT ACA TCC TTG CTA AGC CCC ACT CCG   | 103 |
| Ala Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro   |     |
| -15 -10 -5                                                        |     |
| GCT ACA GCT CTT GCT GTC AGA TAC GCA TCC AAG AAG TCG GGT GGT AGC   | 151 |
| Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser   |     |
| 1 5 10                                                            |     |
| TCC AAA AAC CTC GGT GGA AAG TCA TCA GGC AGA CGC CAA GGC ATT AAG   | 199 |
| Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys   |     |
| 15 20 25                                                          |     |
| AAA ATG GAA GGT CAC TAT GTT CAT GCT GGG AAC ATC ATT GCA ACA CAG   | 247 |
| Lys Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln   |     |
| 30 35 40 45                                                       |     |
| CGC CAT TTC CGC TGG CAC CCA GGT GCC CAT GTG GGT GTT GGG AAG VNT   | 295 |
| Arg His Phe Arg Trp His Pro Gly Ala His Val Gly Val Gly Lys Xaa   |     |
| 50 55 60                                                          |     |
| AAA TGT CTG TAT GCC CTG GAA GAG GGG ATA GTC CGC TAC ACT AAG GAG   | 343 |
| Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu   |     |
| 65 70 75                                                          |     |
| GTC TAC GTG CCT CAT CCC AGA AAC ACG GAG GCT GTG GRT CTG ATC ACC   | 391 |

Val Tyr Val Pro His Pro Arg Asn Thr Glu Ala Val Xaa Leu Ile Thr  
80 85 90

AGG CTG HYC AAG GGT GCT GTG CTC TAC AAG ACT TTT GTC ACG TGG TTC 439  
Arg Leu Xaa Lys Gly Ala Val Leu Tyr Lys Thr Phe Val Thr Trp Phe  
95 100 105

CTG 442  
Leu  
110

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 3..347  
id W81335  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 381..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 376..421  
id W81335  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 352..389
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 346..383  
id W81335  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..234  
id AA156841

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 257..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 233..402  
id AA156841  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..233  
id AA151036  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 232..402  
id AA151036  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 16..413  
id W69555  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..177  
id W81261  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 171..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 162..310  
id W81261  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 325..419  
id W81261  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 21..95
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq AVTSLLSPTPATA/LA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

GGAAGTGAGT GATCGAAAGC ATG GCG TCG GTG GTG TTG GCG CTG AGG ACC CGG 53
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg
 -25 -20 -15

ACA GCC GTT ACA TCC TTG CTA AGC CCC ACT CCG GCT ACA GCT CTT GCT 101
Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala
 -10 -5 1

GTC AGA TAC GCA TCC AAG AAG TCG GGT GGT AGC TCC AAA AAC CTC GGT 149
Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly
 5 10 15

GGA AAG TCA TCA GGC AGA CGC CAA GGC ATT AAG AAA ATG GAA GGT CAC 197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His
 20 25 30

TAT GTT CAT GCT GGG AAC ATC ATT GCA ACA CAG CGC CAT TTC CGC TGG 245
Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp
 35 40 45 50

CAC CCA GGT GCC CAT GTG GGT GTT GGG AAG AAT AAA TGT CTG TAT GCC 293
His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala
 55 60 65

CTG GAA GAG GGG ATA VWC CGC TAC ACT AAG GAG GTC TAC GTG CCT CAT 341
Leu Glu Glu Gly Ile Xaa Arg Tyr Thr Lys Glu Val Tyr Val Pro His
 70 75 80

CCC AGA AAC ACA GAG GCT GTG GAT CTG ATC ACC AGG CTG CCC AAG GGT 389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly
 85 90 95

GCT GTG CTC TAC AAG ACT TTT GTC CAC GTG GTT CCT 425
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro
 100 105 110

```

## (2) INFORMATION FOR SEQ ID NO: 209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 89..321  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 334..391  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 40..88  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..50
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..44  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 94..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 78..313  
id H72445  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 32..79  
id H72445  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 15..50  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..36  
id H72445  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 364..393  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 349..378  
id H72445  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 47..298  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 62..313  
id AA083574  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 296..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 312..345  
id AA083574  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 97..320  
id AA157676  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 12..99  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 3..90  
id AA157676  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 342..399  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 333..390  
id AA157676  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 94..329  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 86..321  
 id R70112  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 47..94  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 40..87  
 id R70112  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 111..281  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.3  
 seq AIALATVLFLLGA/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

ATGAGTGGCA CTTAAGCGGG CCATGCCATG CAACCTTGGG CGCTGCCAAC CGTGGGCGAG 60
CTCTGGGTGT GCGGGCGGCC TGGCGCGGCG CTCCGCTGTG TCAGCGTGTT ATG ATG 116
 Met Met
CCG TCC CGT ACC AAC CTG GCT ACT GGA ATC CCC AGT AGT AAA GTG AAA 164
Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys Val Lys
-55 -50 -45 -40
TAT TCA AGG CTC TCC AGC ACA GAC GAT GGC TAC ATT GAC CTT CAG TTT 212
Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu Gln Phe
-35 -30 -25
AAG AAA ACC CCT CCT AAG ATC CCT TAT AAG GCC ATC GCA CTT GCC ACT 260
Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu Ala Thr
-20 -15 -10
GTG CTG TTT TTG ATT GGC GCC TTT CTC ATT ATT ATA GGC TCC CTC CTG 308
Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser Leu Leu
-5 1 5
CTG TCA GGC TAC ATC AGC AAA GGG GGG GCA GAC CGG GCC GTT CCA GTG 356
Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val Pro Val
10 15 20 25
CTG ATC ATT GGC ATT CTG GTG TTC CTA CCC GGA TTT TAC CAC 398
Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
30 35

```

## (2) INFORMATION FOR SEQ ID NO: 210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 12..344  
id W22200  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..330  
id R87595  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 110..286  
id R88526  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..112
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..112  
id R88526  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 96..309  
id AA031849  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..112
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91  
region 7..91  
id AA031849  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 111..351  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 49..289  
id T08643  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..114  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..53  
id T08643  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 242..286  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```
GAAAATTGAA ACTGAGTGGC CCACGATGGG AAGASGGGAA AGCCCAGGGG TACAGGAGGC 60
CTCTGGGTGA AGGCAGAGGC TAACATGAGG TTCGGAGCGA CCTTGGCCGT TGGCCTGACC 120
ATCTTTGTGC TGTCTGTCGT CACTATCATC ATCTGCTTCA CCTGCTCCTG CTGCTGCCTT 180
TACAAGACGT GCCGCCGACC ACGTCCGGTT GTCACCACCA CCACATCCAC CACTGTGGTG 240
C ATG CCC CTT ATC CTC AGC CTC CAA GTG TGC CGC CCA GCT ACC CTG GAC 289
 Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
 -15 -10 -5 1

CAA GCT ACC AGG GCT ACC ACA CCA TGC CGC CTC AGC CAG GGA TGC CAG 337
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
 5 10 15

CAG CAC CCT ACN NAC CAG 355
Gln His Pro Thr Xaa Gln
 20
```

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 49..395

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 12..358  
id W22200  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 52..383

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..332  
id R87595  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..317

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 110..286  
id R88526  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 31..142

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..112  
id R88526  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 148..361

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 96..309  
id AA031849  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 58..142

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 7..91  
id AA031849  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 141..395  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 49..303  
                           id T08643  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 93..144  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 2..53  
                           id T08643  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 272..316  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.6  
                           seq LILSLQVCRPATL/DQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```

AGATTGCTT TCTTTTCTC CAAAAGGGGA GGAAATTGAA ACTGAGTGGC CCACGATGGG 60
AAGAGGGGAA AGCCCAGGGG TACAGGAGGC CTCTGGGTGA AGGCAGAGGC TAACATGGGG 120
TTCGGAGCGA CCTTGCCCGT TGGCCTGACC ATCTTTGTGC TGTCTGTCGT CACTATCATC 180
ATCTGCTTCA CTGCTCCTG CTGCTGCCTT TACAAGACGT GCCGCCGACC ACGTCCGGTT 240
GTCACCACCA CCACATCCAC CACTGTGGTG C ATG CCC CTT ATC CTC AGC CTC 292
 Met Pro Leu Ile Leu Ser Leu
 -15 -10

CAA GTG TGC CGC CCA GCT ACC CTG GAC CAA GCT ACC AGG GCT ACC ACA 340
Gln Val Cys Arg Pro Ala Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr
 -5 1 5

CCA TGC CGC CTC AGC CAG GGA TGC CAG CAG CAC CCT ACC CAA TGC AGT 388
Pro Cys Arg Leu Ser Gln Gly Cys Gln Gln His Pro Thr Gln Cys Ser
 10 15 20

ACC CAC CTT GGG 400
Thr His Leu Gly
 25

```

## (2) INFORMATION FOR SEQ ID NO: 212:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 175..443

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 152..420  
id AA146275  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 175..443

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 152..420  
id AA146400  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 199..402

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2  
seq GVLLLLSSIHFQC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATTTTCAAG ACCGTACTAG GTAGATGGTC AATTAGAGTT CCCAGGGTTT GAAGCCTGTA  | 60  |
| ACTGCTGCCG CCGCTCAAGC CCTCCAGAGC ATTGCTACGG CTGCTGCCCT TGTACTACTA | 120 |
| CCTCCAAATA CGTTCTTGCT GGTAGTGGCG GCAGCAGGAC CAATTACCTC TTTTGTGCTC | 180 |
| TCCCTCGAGA AGCTCCAG ATG GCG TCT TCC GTG GGC AAC GTG GCC GAC AGC   | 231 |
| Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser                       |     |
| -65 -60                                                           |     |
| ACA GAA CCA ACG AAA CGT ATG CTT TCC TTC CAA GGG TTA GCT GAG TTG   | 279 |
| Thr Glu Pro Thr Lys Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu   |     |
| -55 -50 -45                                                       |     |
| GCA CAT CGA GAA TAT CAG GCA GGA GAT TTT GAG GCA GCB GAG AGA CAC   | 327 |
| Ala His Arg Glu Tyr Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His   |     |
| -40 -35 -30                                                       |     |
| TGC ATG CAG CTC TGG AGA CAA GAG CCA GAC AAT ACT GGT GTG CTT TTA   | 375 |
| Cys Met Gln Leu Trp Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu   |     |
| -25 -20 -15 -10                                                   |     |
| TTA CTT TCA TCT ATA CAC TTC CAG TGT CGA AGG CTG GAC AGA TCT GCT   | 423 |
| Leu Leu Ser Ser Ile His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala   |     |
| -5 1 5                                                            |     |



CAC TTT AGC ACT CTG GCA  
His Phe Ser Thr Leu Ala  
10

441

## (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 43..218  
id AA134795  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 268..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 248..359  
id AA134795  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..65
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..47  
id AA134795  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 43..228  
id AA134712  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..379
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 225..361  
id AA134712  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..65  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..47  
id AA134712  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 48..329  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq VILQLQLFLFDVLQ/KT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATTTGATAGG CGCCGGGCAG CTGAGCTGGT AGGAGGACCA GACGGGG ATG TTC GGC | 56  |
| Met Phe Gly                                                     |     |
| TCC GCC CCC CAG CGT CCC GTG GCC ATG ACG ACC GCT CAG AGG GAC TCC | 104 |
| Ser Ala Pro Gln Arg Pro Val Ala Met Thr Thr Ala Gln Arg Asp Ser |     |
| -90 -85 -80                                                     |     |
| CTG TTG TGG AAG CTC GCG GGG TTG CTG CGG GAG TYY GGG GAT GTG GTC | 152 |
| Leu Leu Trp Lys Leu Ala Gly Leu Leu Arg Glu Xaa Gly Asp Val Val |     |
| -75 -70 -65 -60                                                 |     |
| CTG TCT GGC TGT AGC ACC CTG AGC CTG CTG ACT CCC ACA CTG CAA CAG | 200 |
| Leu Ser Gly Cys Ser Thr Leu Ser Leu Leu Thr Pro Thr Leu Gln Gln |     |
| -55 -50 -45                                                     |     |
| CTG AAC CAC GTA TTT GAG CTG CAC CTG GGG CCA TGG GGC CCT GGC CAG | 248 |
| Leu Asn His Val Phe Glu Leu His Leu Gly Pro Trp Gly Pro Gly Gln |     |
| -40 -35 -30                                                     |     |
| ACA GGC TTT GTG GCT CTG CCC TCC CAT CCT GCC GAC TCC CCT GTT ATT | 296 |
| Thr Gly Phe Val Ala Leu Pro Ser His Pro Ala Asp Ser Pro Val Ile |     |
| -25 -20 -15                                                     |     |
| CTT CAG CTT CAG TTT CTC TTC GAT GTG CTG CAG AAA ACA CTT TCA CTC | 344 |
| Leu Gln Leu Gln Phe Leu Phe Asp Val Leu Gln Lys Thr Leu Ser Leu |     |
| -10 -5 1 5                                                      |     |
| AAG CTG GTC CAT GTT GCT GGT CCT GGC CCC ACA                     | 377 |
| Lys Leu Val His Val Ala Gly Pro Gly Pro Thr                     |     |
| 10 15                                                           |     |

## (2) INFORMATION FOR SEQ ID NO: 214:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 61..312  
id N23581  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..77  
id N23581  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 328..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 310..369  
id N23581  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 119..292  
id AA088606  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 328..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 290..349  
id AA088606  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 62..118

id AA088606  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 13..64  
id AA088606  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(47..331)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 234..518  
id HSGT511  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..387)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 177..236  
id HSGT511  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 73..314  
id W89716  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 330..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 314..371  
id W89716  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 118..350  
id W42358  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 330..387
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 350..407  
id W42358  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 120..377  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq LILVGTSKHAVFG/KI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```
AGTACATCCG GCGAGTAGCT GCGGGTCCCG GGTGCTGCTG GTTAGTGTGC TCTGAGGGAG 60
GGTCCGAGCC AGCCGCTGTT TTGCCGAGAG AGCCCCTCAG GCCGTAGTAA GCATTAATA 119
ATG TCT TTC ATC TTT GAG TGG ATC TAC AAT GGC TTC AGC AGT GTG CTC 167
Met Ser Phe Ile Phe Glu Trp Ile Tyr Asn Gly Phe Ser Ser Val Leu
-85 -80 -75

CAG TTC CTA GGA CTG TAC AAG AAA TCT GGA AAA CTT GTA TTC TTA GGT 215
Gln Phe Leu Gly Leu Tyr Lys Lys Ser Gly Lys Leu Val Phe Leu Gly
-70 -65 -60 -55

TTG GAT AAT GCA GGC AAA ACC ACT CTT CTT CAC ATG CTC AAA GAT GAC 263
Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp
-50 -45 -40

AGA TTG GGC CAA CAT GTT CCA ACA CTA CAT CCG ACA TCA GAA GAG CTA 311
Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
-35 -30 -25

ACA ATT GCT GGA ATG ACC TTA CAA CTT TTG ATC TTG GTS GGC ACG AGC 359
Thr Ile Ala Gly Met Thr Leu Gln Leu Leu Ile Leu Val Gly Thr Ser
-20 -15 -10

AAG CAC GTC GCG TTT GGA AAA ATT ATC 386
Lys His Val Ala Phe Gly Lys Ile Ile
-5 1
```

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 74..179  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 78..183  
id W42807  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 181..266  
id W42807  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 1..74  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 4..77  
id W42807  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 262..291  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 268..297  
id W42807  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 78..321  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 54..297  
id W44615  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 28..61  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..34  
id W44615  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 55..321  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..267  
id W69940  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 57..255  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..199  
id W16769  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 255..321  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 198..264  
id W16769  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..189  
id N46069  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 222..290  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 185..253  
id N46069  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 196..300  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq WYSTVGLLPPVRA/MS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```
AAAGACGCTC ACGGGCGCGC GGACTATCGG GCGGCTAGGC TCTCTGAGGA GGCTGCCACA 60
GTGAAGCAAC CGTGACAAGT GGTGCCCCGAC CAGGGACCTG AACGAGGAAG GTCTGCCAGA 120
GCAGAGAAAG TGAAACTGAT CAGACGAACT ACGAACCCCT GGACGGGAGA GTCTGCCGGC 180
GGAGAATATA AGGAG ATG GAC AAA CCG TGT GGG TGC CCT CCA GGT GTG TGT 231
 Met Asp Lys Pro Cys Gly Cys Pro Pro Gly Val Cys
 -35 -30 -25
GAC CAT GGA ACG GGA GAC CGG AGG GAT CCA TGG TAT TCA ACC GTG GGC 279
Asp His Gly Thr Gly Asp Arg Arg Asp Pro Trp Tyr Ser Thr Val Gly
 -20 -15 -10
CTG TTA CCT CCA GTA CGA GCC ATG AGC CAG CGG AAT CTG AAT 321
```

Leu Leu Pro Pro Val Arg Ala Met Ser Gln Arg Asn Leu Asn  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 161..327  
id H07981  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..211
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 2..155  
id H07981  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 214..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 193..355  
id R59645  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 88..188  
id R59645  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 9..88



id R59645  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 163..369  
id H19239  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 59..164  
id H19239  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 2..51  
id H19239  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..178  
id AA096397  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 337..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 296..330  
id AA096397  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 237..266
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 203..232  
id AA096397  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 212..345
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 145..278  
id W05578  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 125..187  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 59..121  
id W05578  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 68..124  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..57  
id W05578  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 25..132  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq ARALAALVPGVTQ/VD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGTTTCCGGT TCGCCTCCGG AGCC ATG GCG GCG GCA CTG AAG TGT CTA CTG  | 51  |
| Met Ala Ala Ala Leu Lys Cys Leu Leu                             |     |
| -35 -30                                                         |     |
| ACA TTA GGA AGA TGG TGC CCC GGC CTT GGA GTG GCT CCC CAG GCC CGG | 99  |
| Thr Leu Gly Arg Trp Cys Pro Gly Leu Gly Val Ala Pro Gln Ala Arg |     |
| -25 -20 -15                                                     |     |
| GCG CTC GCC GCC TTA GTA CCC GGA GTG ACC CAG GTA GAT AAC AAG TCC | 147 |
| Ala Leu Ala Ala Leu Val Pro Gly Val Thr Gln Val Asp Asn Lys Ser |     |
| -10 -5 1 5                                                      |     |
| GGT TTC CTG CAG AAG AGG CCT CAT CGC CAG CAC CCT GGC ATC CTA AAG | 195 |
| Gly Phe Leu Gln Lys Arg Pro His Arg Gln His Pro Gly Ile Leu Lys |     |
| 10 15 20                                                        |     |
| CTG CCG CAC GTG CGG CTG CCA CAG GCA CTG GCT AAC GGT GCC CAG TTA | 243 |
| Leu Pro His Val Arg Leu Pro Gln Ala Leu Ala Asn Gly Ala Gln Leu |     |
| 25 30 35                                                        |     |
| TTG CTA CTT GGG AGC GCT GGG CCC ACT ATG GAG AAT CAG GTG CAA ACA | 291 |
| Leu Leu Leu Gly Ser Ala Gly Pro Thr Met Glu Asn Gln Val Gln Thr |     |
| 40 45 50                                                        |     |
| CTG ACC AGT TAT CTC TGG AGC AGA CAT TTG CCT GTA GAG CCA GAS GAG | 339 |
| Leu Thr Ser Tyr Leu Trp Ser Arg His Leu Pro Val Glu Pro Xaa Glu |     |
| 55 60 65                                                        |     |

TTG CAA AGA CGG GCT ARG CAT CTT GAG AAA AAA TTC CTG GAA AAC CCA 387  
Leu Gln Arg Arg Ala Xaa His Leu Glu Lys Lys Phe Leu Glu Asn Pro  
70 75 80 85

GAC TTA TCT CAG ACA GAG GAG AAA CTT CGT GGA GCA GGG 426  
Asp Leu Ser Gln Thr Glu Glu Lys Leu Arg Gly Ala Gly  
90 95

## (2) INFORMATION FOR SEQ ID NO: 217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 160..350  
id AA045902  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 24..107  
id AA045902  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 100..149  
id AA045902  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 13..159  
id H45858  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 184..282  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 170..268  
id H45858  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 281..376  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 268..363  
id H45858  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 5..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 22..147  
id W42908  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 184..267  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 200..283  
id W42908  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..361  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 325..381  
id W42908  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 140..189  
id W42908  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 184..376  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 129..321  
id N40684  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 56..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..118  
id N40684  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 204..336  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 267..399  
id AA005400  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 58..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 120..235  
id AA005400  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 31..336  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9  
seq TVMSALSVAPSKA/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

|           |            |            |      |     |     |     |     |     |     |     |     |
|-----------|------------|------------|------|-----|-----|-----|-----|-----|-----|-----|-----|
| GAGTGTCTT | GCGCGTGGAT | CCGAGCGACC | ATG  | GTG | GCC | CGG | GTG | TGG | TCG | CTG | 54  |
|           | Met        | Val        | Ala  | Arg | Val | Trp | Ser | Leu |     |     |     |
|           |            |            | -100 |     |     |     |     |     |     | -95 |     |
| ATG       | AGG        | TTC        | CTC  | ATC | AAG | GGA | AGT | GTG | GCT | GGG | 102 |
| Met       | Arg        | Phe        | Leu  | Ile | Lys | Gly | Ser | Val | Ala | Gly |     |
|           |            |            | -90  |     |     |     |     |     |     | -85 |     |
|           |            |            |      |     |     |     |     |     |     |     | -80 |
| GTG       | TAC        | GAC        | CAG  | GAG | CTG | CTG | GGG | CCC | AGC | GAC | 150 |
| Val       | Tyr        | Asp        | Gln  | Glu | Leu | Leu | Gly | Pro | Ser | Asp |     |
|           |            |            | -75  |     |     |     |     |     |     |     | -65 |
| CTA       | CAG        | AAG        | GCT  | GGG | GAG | GTG | GTC | CCC | CCC | GCC | 198 |
| Leu       | Gln        | Lys        | Ala  | Gly | Glu | Val | Val | Pro | Pro | Ala |     |
|           |            |            | -60  |     |     |     |     |     |     |     | -50 |
|           |            |            |      |     |     |     |     |     |     |     | -50 |
| CAG       | TAC        | GTG        | TGT  | CAG | CAG | ACA | GGC | CTG | CAG | ATA | 246 |
| Gln       | Tyr        | Val        | Cys  | Gln | Gln | Thr | Gly | Leu | Gln | Ile |     |
|           |            |            | -45  |     |     |     |     |     |     |     | -35 |
|           |            |            |      |     |     |     |     |     |     |     |     |
| CCT       | CCA        | AAG        | ATT  | TAC | TTT | CCC | ATC | CGT | GAC | TCC | 294 |
| Pro       | Pro        | Lys        | Ile  | Tyr | Phe | Pro | Ile | Arg | Asp | Ser |     |
|           |            |            | -30  |     |     |     |     |     |     |     | -20 |
|           |            |            |      |     |     |     |     |     |     |     | -15 |

ATG ACG GTG ATG TCA GCT CTG TCG GTG GCC CCC TCC AAG GCC CGC GAG 342  
Met Thr Val Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu  
-10 -5 1  
TAC TCC AAG GAG GGC TGG GAG TAT GTG AAG GCG CTT GGG 381  
Tyr Ser Lys Glu Gly Trp Glu Tyr Val Lys Ala Leu Gly  
5 10 15

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..204  
id AA248187  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 196..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 185..271  
id AA248187  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 302..350
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 289..337  
id AA248187  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..338
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 11..341  
id T93683  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..295  
id AA015679  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 398..445
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq ELQNLXSLQGSQA/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```
AGTTTGTAGC GGACAACATG GCGGCCTTCA TGCTGGGCTC GCTGCTGCGG ACGTTCAAGC 60
AGATGGTTCC TTCATCAGCT TCAGGCCAAG TTCGAAGTCA CTATGTAGAC TGGAGAATGT 120
GGCGCGATGT GAAGAGACGA AAAATGGCCT ATGAATACGC AGATGAGAGG CTACGTATTA 180
ATTCACTCAG GAAGAATACC ATTTTGCCAA AAATTCTTCA GGATGTGGCT GATGAAGAAA 240
TTGCTDHCCT CCCCCGGGAT AGCTGTCCTG TTAGAATCAG AAATCGGTGT GTTATGACGT 300
CCCGTCCGCG TGGTGTGAAG CGGCGCTGGA GGCTTAGTCG TATAGTCTTC CGTCACTTAG 360
CTGACCATGG GCAACTTTCT GGGATCCAGC GAGCGAC ATG GTA AAT GAG CTC CAG 415
 Met Val Asn Glu Leu Gln
 -15

AAC CTA TNG AGC TTG CAG GGA AGC CAA GCT TGC AGT TCC AGC AAG CAA 463
Asn Leu Xaa Ser Leu Gln Gly Ser Gln Ala Cys Ser Ser Ser Lys Gln
-10 -5 1 5

AGA TTT 469
Arg Phe
```

## (2) INFORMATION FOR SEQ ID NO: 219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 122..240  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 102..220  
id T30988  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..112  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..92  
id T30988  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 122..225  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 110..213  
id T30974  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 13..112  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..100  
id T30974  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 122..240  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 84..202  
id HSC0CC031  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 39..112  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..74  
id HSC0CC031  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 122..240  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 84..202  
id HSC0CD031  
est



## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 39..112  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..74  
id HSC0CD031  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..240  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..117  
id R56565  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 80..151  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9  
seq FFFSIQPFLLPCSS/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```
AACACACTCC CTCTCTCTCT CTTTTTAGCA GCAACATACA AGCCGGCCAT ATTAGAGAGA 60
TGGAAATAAA GCTTCCTTA ATG TTG TAT ATG TCT TTG AAG TAC ATC CGT GCA 112
 Met Leu Tyr Met Ser Leu Lys Tyr Ile Arg Ala
 -20 -15

TTT TTT TTT AGC ATC CAA CCA TTC CTC CCT TGT AGT TCT CGC CCC CTC 160
Phe Phe Phe Ser Ile Gln Pro Phe Leu Pro Cys Ser Ser Arg Pro Leu
 -10 -5 1

AAA TCA CCC TCT CCC GTA GCC CAC CCG ACT AAC ATC TCA GTC TCT GAA 208
Lys Ser Pro Ser Pro Val Ala His Pro Thr Asn Ile Ser Val Ser Glu
 5 10 15

AAT GCA CAG AGA TGC CTN NCT ACC TCG CCC TGG 241
Asn Ala Gln Arg Cys Leu Xaa Thr Ser Pro Trp
 20 25 30
```

## (2) INFORMATION FOR SEQ ID NO: 220:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..411
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 167..398  
id N27721  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 38..102  
id N27721  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 99..155  
id N27721  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 202..399  
id N40054  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 73..137  
id N40054  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 134..190  
id N40054  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 213..292

id W25483  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 144..201  
id W25483  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 85..133  
id W25483  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 194..292  
id C17967  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..111
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 65..124  
id C17967  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 125..182  
id C17967  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 280..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 293..354  
id C17967  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..411
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90  
region 273..504  
id AA032534  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 107..168  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 200..261  
id AA032534  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 110..346  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9  
seq WVIVLTSWITIFQ/IY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

ACATAACTGA AAGTAGCTAA GGCACCCCAG CCGGAGGAAG TGAGCTCTCC TGGGTCAAGG 60
CTTGGGTCTT GCCCCGCAGA CCCTTGGGAC GACCCGGCCC CAGCGCAST ATG AAC CTG 118
 Met Asn Leu

GAG CGA GTG TCC AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC 166
Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr
-75 -70 -65

CTG GGG GGG TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC 214
Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe
-60 -55 -50 -45

TGG TTC TTC CGA GAG GCC TTC CTT GTC CCA GCC TAC ACA GAA CAG AGC 262
Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser
-40 -35 -30

CAA ATC AAA GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG 310
Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp
-25 -20 -15

GTG ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC 358
Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro
-10 -5 1

CGC TGG GGT GCC CTH GGG GAC TAS CTC TCC TTC ACC ATA CCC CTG GGC 406
Arg Trp Gly Ala Leu Gly Asp Xaa Leu Ser Phe Thr Ile Pro Leu Gly
5 10 15 20

ACC CCT GAC AAC TTC TGC ACA TAC 430
Thr Pro Asp Asn Phe Cys Thr Tyr
25

```

## (2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 418 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 167..382  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 144..359  
                            id T27537  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 27..162  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 2..137  
                            id T27537  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 162..380  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 89..307  
                            id AA057488  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 75..172  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 93  
                            region 1..98  
                            id AA057488  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 175..381  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 72..278  
                            id H10316  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 105..174  
    (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 1..70  
id H10316  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 162..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 60..283  
id T33282  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 104..162  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..59  
id T33282  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 174..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 65..287  
id R14076  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 112..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 1..62  
id R14076  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 122..331  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9  
seq LVFVLLFIFVKRQ/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```
AATTGCCTGC CTGASTCACG TGTCAGGGGG AAGCTGGAAG GCGTCGTTCT CCTTTCCCAG 60
CTCTCCTGCC TGTCCGCCAT GTTTTCAGGC CGGCTCTGGC TTGGTCTTCC CCCGTAAGRA 120
A ATG GCC GGG GAG CTC CAG GGG ACC CAG GCG CCG TCG CTT CGD GGA SCT 169
 Met Ala Gly Glu Leu Gln Gly Thr Gln Ala Pro Ser Leu Arg Gly Xaa
 -70 -65 -60 -55

GGG CTG ACC AGC CAG GAC AGC GGG GTA AAC CCG AAC AAT TCT GYG CGA 217
Gly Leu Thr Ser Gln Asp Ser Gly Val Asn Pro Asn Asn Ser Xaa Arg
```

-50

-45

-40

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GGT | AGG | GAG | GCC | ATG | GCG | TCC | GGC | AGT | AAC | TGG | CTC | TCC | GGG | GTG | AAT | 265 |
| Gly | Arg | Glu | Ala | Met | Ala | Ser | Gly | Ser | Asn | Trp | Leu | Ser | Gly | Val | Asn |     |
|     |     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GTC | GTG | CTG | GTG | ATG | GCC | TAC | GGG | AGC | CTG | GTG | TTT | GTA | CTG | CTA | TTT | 313 |
| Val | Val | Leu | Val | Met | Ala | Tyr | Gly | Ser | Leu | Val | Phe | Val | Leu | Leu | Phe |     |
|     |     | -20 |     |     |     |     | -15 |     |     |     | -10 |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| ATT | TTT | GTG | AAG | AGG | CAA | ATC | ATG | CGC | TTT | GCA | ATG | AAA | TCT | CGA | AGG | 361 |
| Ile | Phe | Val | Lys | Arg | Gln | Ile | Met | Arg | Phe | Ala | Met | Lys | Ser | Arg | Arg |     |
|     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GGA | CCT | CAT | GTC | CCT | GTR | GGR | NCA | CAA | TGC | CCC | CAA | KGT | TGC | TAC | AAC | 409 |
| Gly | Pro | His | Val | Pro | Val | Gly | Xaa | Gln | Cys | Pro | Gln | Xaa | Cys | Tyr | Asn |     |
|     |     |     |     | 15  |     |     |     | 20  |     |     |     |     | 25  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TAT | CTG | TAT |     |     |     |     |     |     |     |     |     |     |     |     |     | 418 |
| Tyr | Leu | Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 91..360  
id C17648  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 4..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..104  
id C17648  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 93..262

id W07727  
est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 260..362  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 261..363  
 id W07727  
 est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 2..56  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 4..58  
 id W07727  
 est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 58..88  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 59..89  
 id W07727  
 est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 94..251  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 95..252  
 id W00492  
 est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 2..58  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 4..60  
 id W00492  
 est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 253..311  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 255..313  
 id W00492  
 est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 308..342  
 (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 97  
region 311..345  
id W00492  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..362  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 64..366  
id N29017  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..64  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 8..70  
id N29017  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 94..359  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 121..386  
id N31560  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 116..283  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9  
seq FACVPGASPTTLA/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

```
AAACGGAGGC AGGTTGGAGC CGCTGCCGTC GCCATGACCC GCGGTAACCA GCGTGAGCTC 60
GCCCCGCCAGA AGAATATGAA AAAGCAGAGC GACTCGGTTA AGGGAAAGCG CCGAG ATG 118
 Met
ACG GGC TTT CTG CTG CCG CCC GCA AGC AGA GGG ACT CGG AGA TCA TGC 166
Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser Cys
-55 -50 -45 -40
AGC AGA AGC AGA AAA AGG CAA ACG AGA AGA AGG AGG AAC CCA AGT AGC 214
Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser Ser
-35 -30 -25
TTT GTG GCT TCG TGT CCA ACC CTC TTG CCC TTC GCC TGT GTG CCT GGA 262
Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro Gly
-20 -15 -10
GCC AGT CCC ACC ACG CTC GCG TTT CCT CCT GTA GTG CTC ACA GGT CCC 310
Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly Pro
```

-5

1

5

AGC ACC GAT GGC ATT CCC TTT GCC CTG AGT CTG CAG MGG GTC CCT TTT 358  
Ser Thr Asp Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro Phe  
10 15 20 25

GTG 361  
Val

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..459)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 565..794  
id HSZ78357  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..205)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 818..1021  
id HSZ78357  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..389
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 310..337  
id AA052404  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 92..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 62..175  
id H75454  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 30..94  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 1..65  
 id H75454  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 230..307  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.9  
 seq VLCTNQVLITARA/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

```

AACTTCCAAG TTGTAGTGTT GTTGTTTTCA GCCTGCTGCT GCTGCTGCTA TTGCGGCTAG 60
GGGAACCGTC GTGGGAAGG ATGGTGTGCG AAAAATGTGA AAAGAACTT GGTACTGTTA 120
TCACTCCAGA TACATGGAAA GATGGTGCTA GGAATACCAC AGAAAGTGGT GGAAGAAAGC 180
TGAATGAAAA TAAAGCTTTG RCTTCAAAAA AAGCCAGAAT TGAWCCATA ATG GAA GAA 238
 Met Glu Glu
 -25

WTA AGT KCT CCA CTT GTA GAA TTT GTA AAA GTT TTG TGC ACC AAC CAG 286
Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
 -20 -15 -10

GTT CTC ATT ACT GCC AGG GCT GTG CCT ACA AAA AAG GCA TCT GTG CGA 334
Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
 -5 1 5

TGT GTG GMA AAA AGG TTT TGG ATA CCA AAA ACT ACA AGC AAA CAT CTG 382
Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
 10 15 20 25

TCT AGA TGT ATT GAT GGA ATT TCT GGC TTT CTA AAT GAT TTT ACT TTC 430
Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
 30 35 40

TGC CTT GAA TTT TCA AGG CAT AGA TGT 457
Cys Leu Glu Phe Ser Arg His Arg Cys
 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 224:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 119..361  
id AA242967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..120  
id AA242967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 124..260  
id C18969  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 2..125  
id C18969  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 251..309  
id C18969  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 101..343  
id N40141  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 24..125  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..102  
id N40141  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 125..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 122..326  
id R78319  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 9..125  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 7..123  
id R78319  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(125..367)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 112..354  
id N27018  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(73..125)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 353..405  
id N27018  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 106..156  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq LXXVVFVAPGES/QQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```
ATTCTTTCTT CGCCAGGCTC TCTGCTGACT CAAGTTCTTC AGTTCACGAT CTTCTAGTTG 60
CAGCGATGAG TGCACGAGTG AGATCAAGAT CCAGAGGAAG AGGAG ATG GTC AGG AGG 117
 Met Val Arg Arg
 -15

CTM MCG AWT GTG GTT GCA TTC GTG GCT CCC GGT GAA TCT CAG CAA GAG 165
Leu Xaa Xaa Val Val Ala Phe Val Ala Pro Gly Glu Ser Gln Gln Glu
```

-10

-5

1

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GAA CCA CCA ACT GAC AAT CAG GAT ATT GAA CCT GGA CAA GAG AGA GAA | 213 |
| Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly Gln Glu Arg Glu |     |
| 5 10 15                                                         |     |
| GGA ACA CCT CCG ATC GAA GAA CGT AAA GTA GAA GGT GAT TGC CAG GAA | 261 |
| Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly Asp Cys Gln Glu |     |
| 20 25 30 35                                                     |     |
| ATG GAT CTG GAA AAG ACT CGG AGT GAG CGT GGA GAT GGC TCT GAT GTA | 309 |
| Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp Gly Ser Asp Val |     |
| 40 45 50                                                        |     |
| AAA GAG AAG ACT CCA CCT AAT CVT AAG CAT GCT AAG ACT AAA GAA GCA | 357 |
| Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys Thr Lys Glu Ala |     |
| 55 60 65                                                        |     |
| GGA GAT GGG CCA TTG                                             | 372 |
| Gly Asp Gly Pro Leu                                             |     |
| 70                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 299..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 278..433  
id AA100750  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 133..236  
id AA100750  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..159
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..136  
id AA100750  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 9..355  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..347  
id N68686  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 355..402  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 348..395  
id N68686  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 400..429  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 394..423  
id N68686  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 1..241  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 5..245  
id H24263  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 239..337  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 244..342  
id H24263  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 13..123  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq PIVRLLSCPGTVA/KD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TKTTTTTTTAG CA ATG GCG GTT CCC GGC GTG GGG CTC TTG ACC CGT TTG AAC 51  
Met Ala Val Pro Gly Val Gly Leu Leu Thr Arg Leu Asn

|                                                                 | -35 | -30 | -25 |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| CTG TGT GCC CGG AGA AGA ACT CGA GTC CAG CGG CCT ATC GTC AGG CTT |     |     |     | 99  |
| Leu Cys Ala Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu |     |     |     |     |
|                                                                 | -20 | -15 | -10 |     |
| TTG AGT TGC CCA GGA ACT GTG GCC AAA GAC CTT AGG AGA GAC GAG CAG |     |     |     | 147 |
| Leu Ser Cys Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln |     |     |     |     |
|                                                                 | -5  | 1   | 5   |     |
| CCT TCA GGG AGC GTG GAG ACA GGC TTT GAA GAC AAG ATT CCC AAA AGG |     |     |     | 195 |
| Pro Ser Gly Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg |     |     |     |     |
|                                                                 | 10  | 15  | 20  |     |
| AGA TTC TCG GAG ATG CAA AAT GAA AGA CGA GAA CAG GCA CAG CGG ACT |     |     |     | 243 |
| Arg Phe Ser Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr |     |     |     |     |
|                                                                 | 25  | 30  | 35  | 40  |
| GTT TTA ATA CAT TGC CCA GAG AAA ATC AGT GAA AAC AAG TTT CKK AAA |     |     |     | 291 |
| Val Leu Ile His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys |     |     |     |     |
|                                                                 | 45  | 50  | 55  |     |
| TAT TTA TCC CAA TTT GGA CCT ATT AAT AAT CAT TTC TTC TAT GAA AGC |     |     |     | 339 |
| Tyr Leu Ser Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser |     |     |     |     |
|                                                                 | 60  | 65  | 70  |     |
| TTT GGT CTC TAT GCT GTC GTA GAA TTT TGC CAA AAG GAA AGC ATA GGT |     |     |     | 387 |
| Phe Gly Leu Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly |     |     |     |     |
|                                                                 | 75  | 80  | 85  |     |
| TCA CTG CAG AAT GGG ACT CAT ACT CCA AGC ACG GCC ATG GAG ACT GCA |     |     |     | 435 |
| Ser Leu Gln Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala |     |     |     |     |
|                                                                 | 90  | 95  | 100 |     |
| ATT CCA TTC AGA TCA CGT TCT TCA                                 |     |     |     | 459 |
| Ile Pro Phe Arg Ser Arg Ser Ser                                 |     |     |     |     |
|                                                                 | 105 | 110 |     |     |

## (2) INFORMATION FOR SEQ ID NO: 226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 43..253  
id AA017309



est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 93..124  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 28..59  
 id AA017309  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(126..250)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..125  
 id T52392  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 21..200  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.8  
 seq LVILSLKSQTLDA/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

AGTAAGTCCC CCCGCCTCGC ATG ATG GCT GCG GTG CCG CCG GGC CTG GAG CCG 53
 Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
 -60 -55 -50

TGG AAC CGT GTG AGA ATC CCT AAG GCG GGG AAC CGC AGC GCA GTG ACA 101
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
 -45 -40 -35

GTG CAG AAC CCC GGC GCG GCC CTT GAC CTT TGC ATT GCA GCT GTA ATT 149
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
 -30 -25 -20

AAA GAA TGC CAT CTC GTC ATA CTG TCG CTG AAG AGC CAA ACC TTA GAT 197
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
 -15 -10 -5

GCA GAA ACA GAT GTG TTA TGT GCA GTC CTT TAC AGC AAT CAC AAC AGA 245
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
 1 5 10 15

ATG GGC CGC CAC AAA CCC CAT TTG GCC CTC AAA CAG GTT GAG CAA TGT 293
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys
 20 25 30

TTA AAG CGT TTG ARA AAC ATG AAT TTG GAG GGC GGG 329
Leu Lys Arg Leu Xaa Asn Met Asn Leu Glu Gly Gly
 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 385 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Brain
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 39..385  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 1..347  
                            id AA023764  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 146..385  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 95  
                            region 145..384  
                            id C03036  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 11..80  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 2..71  
                            id C03036  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 39..231  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..193  
                            id R08519  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 232..302  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 94  
                            region 193..263  
                            id R08519  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: 11..109

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8

seq SLVHLLCQNQVLG/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAGTGGCAAG ATG GCG TCC CTG GAT CGG GTG AAG GTA CTG GTG TTG GGA  | 49  |
| Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly             |     |
| -30 -25                                                         |     |
| GAC TCA GGT GTT GGG AAA TCT TCG TTA GTC CAT CTC CTA TGC CAA AAT | 97  |
| Asp Ser Gly Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn |     |
| -20 -15 -10 -5                                                  |     |
| CAA GTG CTG GGA AAT CCA TCA TGG ACT GTG GGC TGC TCA GTG GAT GTC | 145 |
| Gln Val Leu Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val |     |
| 1 5 10                                                          |     |
| AGA GTK CAT GAT TAC AAA GAA GGA ACC CCA GAA GAG AAG ACC TAC TAC | 193 |
| Arg Val His Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr |     |
| 15 20 25                                                        |     |
| ATA GAA TTA TGG GAT GTT GGA GGC TCT GTG GGC AGT GCC AGC AGC GTG | 241 |
| Ile Glu Leu Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val |     |
| 30 35 40                                                        |     |
| AAA AGC ACA AGA GCA GTA TTC TAC AAC TCC GTA AAT GGT ATT ATW NYC | 289 |
| Lys Ser Thr Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa |     |
| 45 50 55 60                                                     |     |
| GTA CAC GAC TTA ACV SAT GGG AAG TCC TCC CAA AAM TTG CGN CGT TGG | 337 |
| Val His Asp Leu Thr Xaa Gly Lys Ser Ser Gln Xaa Leu Arg Arg Trp |     |
| 65 70 75                                                        |     |
| TCA TTG GAA GCT CTC AAC AGG GAT TTG GTG CCA ACT GGA GTC TTG GTG | 385 |
| Ser Leu Glu Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val |     |
| 80 85 90                                                        |     |

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 30..237

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 12..219

id R19497  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 219..253  
id R19497  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..185  
id H75597  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 184..218  
id H75597  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..179  
id H93398  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 178..212  
id H93398  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..173  
id HUM030E11B  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..127
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 118..244  
id AA280273  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 50..142  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq WAFSCGTWLPSRA/EW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```
CGGTCCGCGC CATCAGGCCC GAGATAGCGG CGAGGTCCGC TTTCAGTGT ATG GTT TTC 58
 Met Val Phe
 -30

CCT GCC AAA CGG TTC TGC TTG GTG CCA TCC ATG GAG GGC GTG CGC TGG 106
Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly Val Arg Trp
 -25 -20 -15

GCC TTT TCC TGC GGC ACT TGG CTG CCG AGC CGA GCC GAA TGG CTG CTK 154
Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu Trp Leu Leu
 -10 -5 1

RCA GTG CGA TCG ATT CAG CCC GAG GAG AAG GAG CGC ATT GGC CAG TTC 202
Xaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile Gly Gln Phe
 5 10 15 20

GTC TTT GCC CGG GAC GCT AAG GCA GCC ATG GCT GGT CGT CTG ATG ATA 250
Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg Leu Met Ile
 25 30 35

AGG AAA TTA GTT GCA GAG AAT CGA 274
Arg Lys Leu Val Ala Glu Asn Arg
 40
```

## (2) INFORMATION FOR SEQ ID NO: 229:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Surrenals

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 90..208  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 105..223

id HSC13B041  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 18..115  
id HSC13B041  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 71..189  
id T08849  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..81  
id T08849  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..101
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..83  
id H88132  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 71..139  
id H88132  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 140..190  
id H88132  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..208
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 92..189  
id T33149  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..110  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..92  
id T33149  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 18..99  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..82  
id AA121114  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 158..196  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 141..179  
id AA121114  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 12..89  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ACTTTCCCAA | G   | ATG | GCG | TCG | AAG | ATA | GGT | TCG | AGA | CGG | TGG | ATG | TTG | CAG | 50  |     |
|            | Met | Ala | Ser | Lys | Ile | Gly | Ser | Arg | Arg | Trp | Met | Leu | Gln |     |     |     |
|            | -25 |     |     |     |     |     | -20 |     |     |     |     | -15 |     |     |     |     |
| CTG        | ATC | ATG | CAG | TTG | GGT | TCG | GTG | CTG | CTC | ACA | CGC | TGC | CCC | TTT | TGG | 98  |
| Leu        | Ile | Met | Gln | Leu | Gly | Ser | Val | Leu | Leu | Thr | Arg | Cys | Pro | Phe | Trp |     |
|            | -10 |     |     |     |     |     | -5  |     |     |     |     | 1   |     |     |     |     |
| GGC        | TGC | TTC | AGC | CAG | CTC | ATG | CTG | TAC | GCT | GAG | AGG | GCT | GAG | GCA | CGC | 146 |
| Gly        | Cys | Phe | Ser | Gln | Leu | Met | Leu | Tyr | Ala | Glu | Arg | Ala | Glu | Ala | Arg |     |
|            | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |     |     |     |
| CGG        | AAG | CCC | GAC | ATC | CCA | GTG | CCT | TAC | CTG | TAT | TTC | GAC | ATG | GGG | GCA | 194 |
| Arg        | Lys | Pro | Asp | Ile | Pro | Val | Pro | Tyr | Leu | Tyr | Phe | Asp | Met | Gly | Ala |     |
|            | 20  |     |     |     | 25  |     |     | 30  |     |     |     |     |     | 35  |     |     |
| GCC        | GTG | CTG | TGC | GCG | CGG |     |     |     |     |     |     |     |     |     |     | 212 |
| Ala        | Val | Leu | Cys | Ala | Arg |     |     |     |     |     |     |     |     |     |     |     |
|            |     |     |     |     |     | 40  |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 19..272  
id W52056  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 128..220
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq LAVDSWWLDPGHA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```

AAGAACTGCG TCTCGCGACC CAGGCGCGGG TTCCCGGAGG ACAGCCARCA AGCGATGCTG 60
CCGCCGCCGT TTCCTGATTG GTTGTGGGTG GCTACCTCTT CGTTCTGATT GGCCGCTAGT 120
GAGCAAG ATG CTG AGC AAG GGT CTG AAG CGG AAA CGG GAG GAG GAG GAG 169
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu
 -30 -25 -20

GAG AAG GAA CCT CTG GCA GTC GAC TCC TGG TGG CTA GAT CCT GGC CAC 217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
 -15 -10 -5

GCA GCG GTG GCA CAG GCA CCC CCG GCC GTG GCC TCT AGC TCC CTC TTT 265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
 1 5 10 15

GAC CTC TCA GTG CTC AAG CTC CAC CAC AGC CGC GGG 301
Asp Leu Ser Val Leu Lys Leu His His Ser Arg Gly
 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 231:

## (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 380 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 88..277  
id W02951  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 36..89  
id W02951  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 345..379  
id W02951  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..41
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..36  
id W02951  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 313..344  
id W02951  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..316
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 279..312  
id W02951  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 93..305  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 81..293  
id N40687  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 12..93  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..82  
id N40687  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..381  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 292..363  
id N40687  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 93..305  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 80..292  
id N44828  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..381  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 291..367  
id N44828  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 40..93  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 28..81  
id N44828  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 93..381  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 79..367  
id R91018  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 14..93  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..80  
id R91018  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 93..305  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 80..292  
id W19557  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 13..93  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..81  
id W19557  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..380  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 291..366  
id W19557  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 282..329  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq SLAAPALTLHGHWG/LG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

AAGGAACGAG ATGGCGGTTT TCTGGAGGCT GAGTGCCGTT TCGGGTGCCC TAGGAGGCCG 60  
AGCTCTGTTG CTTCGAACTC CAGTGGTCAG AMCCTGCTCA TATCTCAGCA TTTCTTCAGG 120  
ACCGACCTAT CCCAGAATGG TGTGGAGTGC AGCACATACA CTTGTCACCG AGCCACCATT 180  
CTGGCTCCAA GGCTGCATCT CTCCACTGGA CTAGCGAGAG GGTGTCAGT GTTTTGCTCC 240

TGGGTCTGCT TCCGGCTGCT TATTTGAATC CTTGCTCTGC G ATG GAC TAT TCC CTG 296  
Met Asp Tyr Ser Leu  
-15

GCT GCA GCC CTC ACT CTT CAT GGT CAC TGG GGC CTT GGA CAA GTT GTT 344  
Ala Ala Ala Leu Thr Leu His Gly His Trp Gly Leu Gly Gln Val Val  
-10 -5 1 5

ACT GAC TAT GTT CAT GGG GAT GCC TTG CAG AAA GCT 380  
Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys Ala  
10 15

## (2) INFORMATION FOR SEQ ID NO: 232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 128..338  
id HUM080D04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..134  
id HUM080D04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 348..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 339..399  
id HUM080D04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 407..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 397..435  
id HUM080D04B  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 138..274  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 127..263  
id H29248  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 11..143  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..133  
id H29248  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 273..348  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 263..338  
id H29248  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 348..387  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 339..378  
id H29248  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 382..411  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 374..403  
id H29248  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 138..348  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 123..338  
id HUM179H02B  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 10..143

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..134  
id HUM179H02B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 348..397  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 339..388  
id HUM179H02B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 407..437  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 396..426  
id HUM179H02B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 138..299  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 135..296  
id H73551  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 3..143  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..141  
id H73551  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 292..348  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 290..346  
id H73551  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 402..441  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 407..446  
id H73551  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 138..326  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 94..282  
id W68502  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..143  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..100  
id W68502  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 348..408  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 306..366  
id W68502  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 181..396  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq LSLXASYIFGISG/FE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

|                                                                 |            |            |            |            |            |     |
|-----------------------------------------------------------------|------------|------------|------------|------------|------------|-----|
| AGTTTTTCAGG                                                     | ARATTTGGAA | GCTGCCGCAG | TAGTTGGAGT | CTAAGGACTC | GTGACAATCT | 60  |
| TCGGGTGCCC                                                      | TTCGAGAGAA | AAGGGGAGGA | TGCCACTGGA | GTCATCCTCT | TCAATGCCAC | 120 |
| TATCCTTCCC                                                      | ATCTBYBYTD | RCCCTCRGTA | CCACACAATA | CTAACCCCTC | CCCTNCTCTG | 180 |
| ATG TCT TAC ATC ACC TCC CAG GAG ATG AAG TGT ATT CTT CAC TGG TTT |            |            |            |            |            | 228 |
| Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe |            |            |            |            |            |     |
| -70                                                             |            | -65        |            |            | -60        |     |
| GCC AAT TGG TCA GGT CCC CAG CGT GAA CGT TTC CTA GAG GAC CTG GTA |            |            |            |            |            | 276 |
| Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val |            |            |            |            |            |     |
| -55                                                             |            | -50        |            |            | -45        |     |
| GCT AAG GCA GTG CCA GAA AAA TTA CAA CCA HTG CTG GAT AGT CTG GAG |            |            |            |            |            | 324 |
| Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu |            |            |            |            |            |     |
| -40                                                             |            | -35        |            |            | -30        | -25 |
| CAG CTT AGT GTG TCT GGG GCA GAC GAC CAC CTT CTA TCT TTG WGT GCC |            |            |            |            |            | 372 |
| Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala |            |            |            |            |            |     |
| -20                                                             |            |            |            | -15        |            | -10 |
| AGC TAC ATC TTT GGG ATC AGT GGT TTC GAG GCT GGG GCT GAG CAG GAG |            |            |            |            |            | 420 |
| Ser Tyr Ile Phe Gly Ile Ser Gly Phe Glu Ala Gly Ala Glu Gln Glu |            |            |            |            |            |     |
| -5                                                              |            |            | 1          |            |            | 5   |

CGC AAT GAA TTT GTC AGA CAG TCG  
Arg Asn Glu Phe Val Arg Gln Ser  
10 15

444

## (2) INFORMATION FOR SEQ ID NO: 233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 6..366  
id W31798  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..353  
id AA056667  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 4..342  
id AA131958  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..334  
id H10262  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..406
- (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 99  
region 1..330  
id W95790  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 200..427  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq LIVYLWVVSFIAS/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```
AAGACGAGGT CATGAATCAT GTGACGGTGG CTTGAGGAGG AACCTGTCTT TAAAGCTGTC 60
CCTGAAGTGA CAGCGGAGAG AACCAGGCAG CCCAGAAACC CCAGGCGTGG AGATTGATCC 120
TGCGAGAGAA GGGGGTTCAT CATGGCGGAT GACCTAAAGC GATTCTTGTA TAAAAAGTTA 180
CCAAGTGTTG AAGGGCTCC ATG CCA TTG TTG TGT CAG ATA GAG ATG GAG TAC 232
 Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr
 -75 -70

CTG TTA TTA AAG TGG CAA ATG ACA ATG CTC CAG AGC ATG CTT TGC GAC 280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp
-65 -60 -55 -50

CTG GTT TCT TAT CCA CTT TTG CCC TTG CAA CAG ACC AAG GAA GCA AAC 328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn
 -45 -40 -35

TTG GAC TTT CCA AAA ATA AAA GTA TCA TCT GTT ACT ATA ACA CCT ACC 376
Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr
 -30 -25 -20

AGG TGG TTC MAT TTA ATC GTT TAC CTT TGG GTG GTG AGT TTC ATA GCC 424
Arg Trp Phe Xaa Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala
 -15 -10 -5

AGC AGC AGT 433
Ser Ser Ser
1
```

## (2) INFORMATION FOR SEQ ID NO: 234:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Surrrenals.

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 39..179  
id C15963  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 161..261  
id C15963  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..219
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 22..224  
id W07092  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..239)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 140..377  
id W72958  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 16..255  
id W24219  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 16..253  
id AA040714  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 45..110
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq SVMGVCLLIPGLA/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

AAAGGACCCA GAAGTAGGGT TTTGGCCTAG GTAACGGGGC AGAG ATG TGG TTC GAG 56
 Met Trp Phe Glu
 -20

ATT CTC CCC GGA CTC TCC GTC ATG GGC GTG TGC TTG TTG ATT CCA GGA 104
Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu Leu Ile Pro Gly
-15 -10 -5

CTG GCT ACT GCG TAC ATC CAC ARG TTC ACT AAC CGG GGC AAG GAA AAA 152
Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg Gly Lys Glu Lys
1 5 10

AGG GTT GCT CAT TTT GGG TAT CAC TGG AGT CTG ATG GAA AGA GAT AGG 200
Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met Glu Arg Asp Arg
15 20 25 30

CGC ATC TCT GGA GTT GAT CGT TAC TAT GTG TCA AAG GGT CCA GGG 245
Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys Gly Pro Gly
35 40 45

```

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 162..309  
id AA017973  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 181..328  
id AA021972  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 181..328  
id AA013987  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 204..351  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 168..315  
id AA014054  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 204..351  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 184..331  
id W80073  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 205..342  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq LLVSLVLRXPAKS/TR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```
AGTTTAGCGA CCGGACCCGA AACGGGGAAG TTGTCTTG TGAGAGGTT AGTAAAGCAG 60
CGCGCGCGTC ACCAGAGTCG TTTCTCTTCG GAGTCTTAGG TGATCGAGGG TGTGCCCAGG 120
GGGCGGACTT GTTTGC GCCT CCCGTTCCCT CCCAATTTCC AAACGTGTCA CCCC GGCGCC 180
GACGGCCCTG TGCAGGGGAA GCAG ATG GAG TTC AAG CTG GAG GCT CAT CGC 231
 Met Glu Phe Lys Leu Glu Ala His Arg
 -45 -40

ATC GTC AGC ATC TCT CTG GGC AAG ATC TAC AAC TCG CGG GTC CAG CGC 279
Ile Val Ser Ile Ser Leu Gly Lys Ile Tyr Asn Ser Arg Val Gln Arg
 -35 -30 -25

GGC GGC ATC AAG CTG CAT AAG AAC CTC CTG GTC TCG CTG GTG CTG CGC 327
Gly Gly Ile Lys Leu His Lys Asn Leu Leu Val Ser Leu Val Leu Arg
 -20 -15 -10

ASG CCC GCC AAG TCT ACC CGA GCG GGG 354
Xaa Pro Ala Lys Ser Thr Arg Ala Gly
 -5 1
```

## (2) INFORMATION FOR SEQ ID NO: 236:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..179  
id AA146876  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 214..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 179..333  
id AA146876  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 334..363  
id AA146876  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 15..285  
id AA044109  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 371..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 338..381  
id AA044109  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 307..336

id AA044109  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 27..337  
id H21138  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 347..382  
id H21138  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 14..216  
id AA150025  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 271..332  
id AA150025  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 216..278  
id AA150025  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 332..376  
id AA150025  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..368
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..310  
id N28828  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 370..414  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 311..355  
id N28828  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 94..384  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq IASGLGLXLDWCWT/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```
AATCTAGCCC CGCCCCAGGC GAGGGCGCCG CACCCACACC GCGCTGCGCA GTTTTGTTCT 60
GCTCCAGCTG TTCGAAGGTG ATCCAGACGC AAG ATG GCT GTC CTC TCT AAG GAA 114
 Met Ala Val Leu Ser Lys Glu
 -95

TAT GGT TTT GTG CTT CTA ACT GGT GCT GCC AGC TTT ATA ATG GTG GCC 162
Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala
-90 -85 -80 -75

CAC CTA GCC ATC AAT GTT TCC AAG GCC CGC AAG AAG TAC AAA GTG GAG 210
His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu
 -70 -65 -60

TAT CCT ATC ATG TAC AGC ACG GAC CCT GAA AAT GGG CAC ATC TTC AAC 258
Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn
 -55 -50 -45

TGC ATT CAG CGA GCC CAC CAG AAC ACG TTG GAA GTG TAT CCT CSC TTC 306
Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Xaa Phe
 -40 -35 -30

TTA TTT TTT CTA GCT GTT GGA GGT GTT TAC CAC CCG CGT ATA GCT TCT 354
Leu Phe Phe Leu Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser
 -25 -20 -15

GGC CTG GGC TTG DCN CTG GAT TGT TGG ACG AGT TCT TTA TGC TTA TGG 402
Gly Leu Gly Leu Xaa Leu Asp Cys Trp Thr Ser Ser Leu Cys Leu Trp
-10 -5 1 5

CTA TTA CAC GGG CCG GGG 420
Leu Leu His Gly Pro Gly
 10
```

## (2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 406 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Brain
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 28..227  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..200  
                            id AA074804  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 265..310  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 238..283  
                            id AA074804  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 227..263  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 201..237  
                            id AA074804  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 352..385  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 94  
                            region 328..361  
                            id AA074804  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: complement(259..403)  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 123..272  
                            id N93600  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: complement(85..207)



(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 325..447  
id N93600  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(202..408)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 117..323  
id AA074748  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(116..153)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 375..412  
id AA074748  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(167..202)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 324..359  
id AA074748  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(258..408)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 123..273  
id N93603  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(208..251)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 280..323  
id N93603  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(163..202)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 329..368  
id N93603  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(90..125)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 411..446  
id N93603  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 272..397
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq RIPS LPGSPVCWA/WP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```
AAAAGGAAAG AGGTYSGGAG CGCTCGCGAG ATCTCGGACC ACCCAACCTG AAAGGTGCTT 60
AGGAAGTTGA AAGGCCCAGA GGAGGCCTCC GGGCAAATGG CCGGAGCTGG ACCGACCATG 120
CTGCTACGAG AAGAGAATGG CTGTTGCAGT CGGCGTCAGA GCAGCTCCAG TGCCGGGGAT 180
TCGGACGGAG AGCGCGAGGA CTCGGCGGCT GAGCGCGCCC GACAGCAGCT AGAGGCGCTG 240
CTCAACAAGA CTATGCGCAT TCGCATGACA G ATG GAC GGA CAC TGG TCG GCT 292
 Met Asp Gly His Trp Ser Ala
 -40

GCT TTC TCT GCA CTG ACC GTG ACT GCA ATG TCA TCC TGG GCT CGG CGC 340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35 -30 -25 -20

AGG AGT TCC TCA AGC CGT CGG ATT CCT TCT CTG CCG GGG AGC CCC GTG 388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
 -15 -10 -5

TGC TGG GCC TGG CCA TGG 406
Cys Trp Ala Trp Pro Trp
 1
```

## (2) INFORMATION FOR SEQ ID NO: 238:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Liver

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..207

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 20..171  
id N41898  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 69..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 38..176  
id H69272  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 56..103  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.5  
seq RLLLRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ACTTGACAGG CAGGGAGGGC TAGGCTGTGC ATCCCTCCGC TCGCATTGCA GGGAG ATG | 58  |
| Met                                                              |     |
| GCT CAG CGA CTT CTT CTG AGG AGG TTC CTG GCC TCT GTC ATC TCC AGG  | 106 |
| Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser Arg  |     |
| -15 -10 -5 1                                                     |     |
| AAG CCC TCT CAG GGT CAG TGG CCA CCC CTC ACT TCC AGA GCC CTG CAG  | 154 |
| Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu Gln  |     |
| 5 10 15                                                          |     |
| ACC CCA CAA TGC AGT CCT GGT GGC CTG ACT GTA ACA CCC AAC CCA GCC  | 202 |
| Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro Ala  |     |
| 20 25 30                                                         |     |
| CGG ACG                                                          | 208 |
| Arg Thr                                                          |     |
| 35                                                               |     |

## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..343  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 103..322  
id H72703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 24..135  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 4..115  
id H72703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 357..398  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 336..377  
id H72703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..343  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..337  
id W68324  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 357..391  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 351..385  
id W68324  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..134  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..128  
id AA054941  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 191..283  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 185..277  
id AA054941  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 117..184  
id AA054941  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 361..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 360..397  
id AA054941  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 97..316  
id AA128297  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..134
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..108  
id AA128297  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 330..371  
id AA128297  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(153..300)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 108..255  
id H72704  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(291..343)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 64..116

id H72704  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(101..151)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 259..309  
id H72704  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(357..398)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 9..50  
id H72704  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 311..385
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq FLLLEVSHLLLI/IN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
AGACGTGTTC TTCCGGTGGC GGASGGCGGA TTAGCCTTCG CGGGGCAAAA TGGAGCTCGA 60
GGCCATGAGC AGATATACCA GCCCAGTGAA CCCAGCTGTC TTCCCCCATC TGACCGTGGT 120
GCTTTTGSCC ATTGGCATGT TCTTCACCGC CTGTTTCTTC GTTTACGAGG TCACCTCTAC 180
CAAGTACACT CGTGATATCT ATAAAGAGCT CCTCATCTCC TTAGTGGCCT CACTCTTCAT 240
GGGCTTTGGA GTCCTCTTCC TGCTGCTCTG GGTGCGCATC TACGTGTGAG CACCCAAGGG 300
TAACAACCAG ATG GCT TCA CTG AAA CCT GCT TTT GTA AAT TAC TTT TTT 349
 Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe
 -25 -20 -15

TTA CTG TTG CTG GAA GTG TCC CAC CTG CTG CTC ATA ATA AAT GCA GAA 397
Leu Leu Leu Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu
 -10 -5 1

GGG
Gly
5
400
```

## (2) INFORMATION FOR SEQ ID NO: 240:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..396

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 202..372  
id N40054  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 27..162

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 2..137  
id N40054  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 158..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 134..190  
id N40054  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 15..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 2..133  
id W25483  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..305

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 213..292  
id W25483  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 157..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 144..201  
id W25483  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..124  
id C17967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 194..292  
id C17967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 157..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 125..182  
id C17967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 293..354  
id C17967  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 167..337  
id N27721  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..102  
id N27721  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 99..155



id N27721  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 50..214  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..165  
id T47061  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 226..377  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 177..328  
id T47061  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 156..386  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.5  
seq LFWVIVLTSWITI/FQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```
AAAAACGTCC ATAAGTAAA GTAGCTAAGG CACCCCAGCC GGAGGAAGTG AGCTCTCCTG 60
GGGCGTGTTT GTTCGTGATC CTTGCATCTG TTAAGTAGGG TCAAGGCTTG GGTCTTGCCC 120
CGCAGACCCT TGGGACGACC CGGCCCCAGC GCAAT ATG AAC CTG GAG CGA GTG 173
 Met Asn Leu Glu Arg Val
 -75

TCC AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC CTG GGG GGG 221
Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr Leu Gly Gly
-70 -65 -60

TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC TGG TTC TTC 269
Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe Trp Phe Phe
-55 -50 -45 -40

CGA GAG GCC TTC CTT GTC CCA GCC TAC ACA GAA CAG AGC CAA ATC AAA 317
Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser Gln Ile Lys
 -35 -30 -25

GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG GTG ATA GTG 365
Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp Val Ile Val
 -20 -15 -10

CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC 395
Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
-5 1
```

## (2) INFORMATION FOR SEQ ID NO: 241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 170..205  
id AA090974  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 73..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq AVASSFFCASLFS/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```
ATTTTTTCT TGCTCGTGGG CTCGGACGAG TACGGAGCGC CTGCAGGGAC AGCCTGGATA 60
AAGGCTCACT TG ATG GCT CAG TTG GGA GCA GTT GTG GCT GTG GCT TCC AGT 111
 Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser
 -20 -15 -10

TTC TTT TGT GCA TCT CTC TTC TCA GCT GTG CAC AAG ATA GAA GAG GGA 159
Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly
 -5 1 5

CAT ATT GGG GTA TAT TAC AGA GGC GGT GTG 189
His Ile Gly Val Tyr Tyr Arg Gly Gly Val
 10 15
```

## (2) INFORMATION FOR SEQ ID NO: 242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 16..262  
id AA044042  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 1..33  
id AA044042  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 6..239  
id AA127902  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..216  
id AA056679  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(104..308)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 246..450  
id W93399  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..184  
id H39528  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 122..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4  
seq LVFMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```
GCGAAGGTTG TCGGGATCCG CGGCAGCAGC GGCTGCTTGA GATCTGTTTC TGGGGCCTCT 60
GGCGGTGGCG GCCTGGGGCG GCGCGACGGC TGGTGCGCAG GTACACTGAT GCTGAAGTAC 120
T ATG AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT TTT ATG 169
 Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met
 -25 -20 -15 -10

GTC CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC 217
Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
 -5 1 5

AGC CCT GTT TTC CAA ATA CCT AAA AAC GAC GAC ATT CCT GAG CAA GAT 265
Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
 10 15 20

AGT CTG GGA CTT TCA AAT CTT CAG AAG AGC CAA ATC CAG GGG ATA CTG 313
Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu
 25 30 35
```

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..306
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 33..232  
id AA088487  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 341..409
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq VFCLLSIPTPSA/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```
AGTCGTTGCC ATSGATCCTG GGGACGACTG GCTGGTGGAA TCCTTGCGCT TGTAATCGT 60
ACCAGGATTT CTATGCATTC GACCTGTCAG GAGCCACTCG AGTCCTTGAA TGGATTGATG 120
ACAAAGGAGT CTTTGTGCT GGCTATGAAA GCCTGAAAAA GAATGAAATT CTTCATCTGA 180
AATTACCTCT CAGACTTTCT GTAAAGGAAA ACAAGGGCTT ATTCCCAGAA AGAGATTTCA 240
AAGTGCGCCA TGGAGGATTT TCAGACAGGT CTATCTTTGA TCTAAAGCAT GTGCCACATA 300
CCAGGTATGG TCAATTTTGT GATCCAGCCA TCCACACAGG ATG GGA TGG GAT GGC 355
 Met Gly Trp Asp Gly
 -20

TGC AAA TGC CTG GGG GTA TTC TGC CTC CTC ATC TCC ATT CCC ACC CCC 403
Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile Ser Ile Pro Thr Pro
 -15 -10 -5

TCA GCA CAC CTG 415
Ser Ala His Leu
 1
```

## (2) INFORMATION FOR SEQ ID NO: 244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..451
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 122..417  
id AA085629  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..144
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 14..114  
id AA085629  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..259
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 134..237  
id AA132309  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 47..144  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 29..126  
id AA132309  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 274..314  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 254..294  
id AA132309  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 47..144  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 15..112  
id H35088  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 156..345  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 63..252  
id HUML11153  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 12..365  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq ILAHLRLGLIPIHA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

|                                                                  |              |
|------------------------------------------------------------------|--------------|
| AGAGATTGAA G ATG GCG GCT TCT CAG GCG GTG GAG GAA ATG CGG ACC GCG | 50           |
| Met Ala Ala Ser Gln Ala Val Glu Glu Met Arg Thr Ala              |              |
| -115                                                             | -110         |
| <br>                                                             |              |
| TGG TTC TGG GGG AGT TTG GGG TTC GCA ATG TCC ATA CTA CTG ACT TTC  | 98           |
| Trp Phe Trp Gly Ser Leu Gly Phe Ala Met Ser Ile Leu Leu Thr Phe  |              |
| -105                                                             | -100 -95 -90 |
| <br>                                                             |              |
| CCG GTA ACT ATT CCG GTT ATG ATG ATG CCT GGG ACC AGG RMC GGY TTC  | 146          |
| Pro Val Thr Ile Pro Val Met Met Met Pro Gly Thr Arg Xaa Gly Phe  |              |

|                                                                 | -85 | -80 | -75 |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| GAA GRA AGA AWT TTC CGT GTG GAT GTA GTA CAC ATG GAT GAA AAC TCA |     |     |     | 194 |
| Glu Xaa Arg Xaa Phe Arg Val Asp Val Val His Met Asp Glu Asn Ser |     |     |     |     |
|                                                                 | -70 | -65 | -60 |     |
| CTG GAG TTT GAC ATG GTG GGA ATT GAC GCA GCC ATT GCC AAT GCT TTT |     |     |     | 242 |
| Leu Glu Phe Asp Met Val Gly Ile Asp Ala Ala Ile Ala Asn Ala Phe |     |     |     |     |
|                                                                 | -55 | -50 | -45 |     |
| CGA CGA ATT CTG CTA GCT GAG GTG CCA ACT ATG GCT GTG GAG AAG GTC |     |     |     | 290 |
| Arg Arg Ile Leu Leu Ala Glu Val Pro Thr Met Ala Val Glu Lys Val |     |     |     |     |
|                                                                 | -40 | -35 | -30 |     |
| CTG GTG TAC AAT AAT ACA TCC ATT GTT CAG GAT GAG ATT CTT GCT CAC |     |     |     | 338 |
| Leu Val Tyr Asn Asn Thr Ser Ile Val Gln Asp Glu Ile Leu Ala His |     |     |     |     |
|                                                                 | -25 | -20 | -15 | -10 |
| CGT CTG GGG CTC ATT CCC ATT CAT GCT GAT CCC CGT CTT TTT GAG TAT |     |     |     | 386 |
| Arg Leu Gly Leu Ile Pro Ile His Ala Asp Pro Arg Leu Phe Glu Tyr |     |     |     |     |
|                                                                 | -5  | 1   | 5   |     |
| CGG AAC CAA GGA GAT GAA GAA GGC ACA GAG ATA GAT ACT CTA CAG TTT |     |     |     | 434 |
| Arg Asn Gln Gly Asp Glu Glu Gly Thr Glu Ile Asp Thr Leu Gln Phe |     |     |     |     |
|                                                                 | 10  | 15  | 20  |     |
| CGT CTC CAG GTC AGA TGC ACT CGG                                 |     |     |     | 458 |
| Arg Leu Gln Val Arg Cys Thr Arg                                 |     |     |     |     |
|                                                                 | 25  | 30  |     |     |

## (2) INFORMATION FOR SEQ ID NO: 245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..188
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 45..172  
id AA156837  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 234..316

id AA156837  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 189..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 172..239  
id AA156837  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..64
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..49  
id AA156837  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..206  
id AA196478  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 236..318  
id AA196478  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 207..241  
id AA196478  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 44..209  
id AA181144  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 90  
region 235..317  
id AA181144  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..64  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..48  
id AA181144  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 225..256  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 209..240  
id AA181144  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 185..334  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 169..318  
id AA228369  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 61..184  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 46..169  
id AA228369  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 22..64  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 8..50  
id AA228369  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 15..219  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..205  
id W04828  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 252..334  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 236..318  
                           id W04828  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 341..380  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 323..362  
                           id W04828  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 221..256  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 206..241  
                           id W04828  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 12..242  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
                           seq FEARIALLP LLQA/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ATACTGCGAG T ATG GCG GCG TCA AAG GTG AAA CAG GAC ATG CCT CCG CCG | 50  |
| Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro              |     |
| -75 -70 -65                                                      |     |
| GGG GGC TAT GGG CCC ATC GAC TAC AAA CGG AAC TTR CCG CGT CGA GGA  | 98  |
| Gly Gly Tyr Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly  |     |
| -60 -55 -50                                                      |     |
| CTG TCG GCC TAC ACC ATG CTG GCC ATA GGG ATT GGA ACC CTG ATC TAC  | 146 |
| Leu Ser Gly Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr  |     |
| -45 -40 -35                                                      |     |
| GGG CAC TGG AGC ATA ATG AAG TGG AAC CGT GAG CGC AGG CGC CTA CAA  | 194 |
| Gly His Trp Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln  |     |
| -30 -25 -20                                                      |     |
| ATC GAG GAC TTC GAG GCT CGC ATC GCG CTG TTG CCA CTG TTA CAG GCA  | 242 |
| Ile Glu Asp Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala  |     |
| -15 -10 -5                                                       |     |
| GAA ACC GAC CGG ARG ACC TTG CAG ATG CTT CGG GAG AAC CTG GAG GAG  | 290 |
| Glu Thr Asp Arg Xaa Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu  |     |
| 1 5 10 15                                                        |     |
| GAG GCC ATC ATC ATG MAG GAC GTS CYC GAC TGG AAS GTG GGG RAA KVV  | 338 |
| Glu Ala Ile Ile Met Xaa Asp Val Xaa Asp Trp Xaa Val Gly Xaa Xaa  |     |

20

25

30

GHT GTT CCA CAC AAC CCG CTG GGT GCÇ CCC CTT GAT CGG GGA GCT  
Xaa Val Pro His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala  
35 40 45

383

## (2) INFORMATION FOR SEQ ID NO: 246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 54..267  
id AA027968  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 105..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 94..278  
id N90497  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..108
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..99  
id N90497  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 21..265  
id HSC0SD021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..299

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..259  
                           id T31694  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 116..274  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 61..219  
                           id R38457  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 55..107  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 1..53  
                           id R38457  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 273..307  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 219..253  
                           id R38457  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 164..289  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
                           seq VLFFGTGWIIIDA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AATGCGCGAC TGAGCCGGGT GGATGGTACT GCTGCATCCG GGTGTCTGGA GGCTGTGGCC 60
GTTTTGTTTT CTTGGCTAAA ATCGGGGGGAG TGAGGCGGGC CGGCGCGGCG CGACACCGGG 120
CTCCGGAACC ACTGCACGAC GGGGCTGGAC TGACCTGAAA AAA ATG TCT GGA TTT 175
 Met Ser Gly Phe
 -40
CTA GAG GGC TTG AGA TGC TCA GAA TGC ATT GAC TGG GGG GAA AAG CGC 223
Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp Gly Glu Lys Arg
-35 -30 -25
AAT ACT ATT GCT TCC ATT GCT GCT GGT GTA CTA TTT TTT ACA GGC TGG 271
Asp Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe Phe Thr Gly Trp
-20 -15 -10
TGG ATT ATC ATA GAT GCA GCT GTT ATT TAT CCC ACC CGG 310
Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr Arg

```

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 73..353  
id AA133050  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 42..71  
id AA133050  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 145..290  
id AA159550  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 47..145  
id AA159550  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..394
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 319..374  
id AA159550

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 10..45  
id AA159550  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 225..356
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq LVFLTFLSIPSFV/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```

AAGGTGCTCG TCATGCGCAA TGTGGCGCTG CGGCGGGCGG CAGGGCCTGT GTGTGCTGAG 60
GCGGCTGAGC GGCGGACATG CACACCACAG AGCGTGGCGA TGGAACAGTA ACCGGGCTTG 120
TGAGAGGGCT CTGCAGTATA AACTAGGAGA CAAGATCCAT GGATTCACCG TAAACCAGGT 180
GACATCTGTT CCGGAGCTGT TCCTGACTGC AGTGAAGCTC ACCC ATG ATG ACA CAG 236
 Met Met Thr Gln
GAG CCA GGT ATT TAC ACC TGG CCA GAG AAA ACA CGA ATA ATC TGT TCA 284
Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg Ile Ile Cys Ser
-40 -35 -30 -25
GCG TGC AGT TCC GTA CCA CTC CCA TGG ACA GTA CTG GTG TTC CTC ACA 332
Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu Val Phe Leu Thr
 -20 -15 -10
TTC TTG AGC ATA CCG TCC TTT GTG GGT CTC AGA AAT ATC CGT GCA GAG 380
Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Arg Asn Ile Arg Ala Glu
 -5 1 5
ACC TTT CTT CAA AAT GTT 398
Thr Phe Leu Gln Asn Val
10

```

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(53..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 444..585  
id AA161193  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(227..324)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 311..408  
id AA161193  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..406)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 230..308  
id AA161193  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(408..446)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 188..226  
id AA161193  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..406)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 75..153  
id R06283  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(275..324)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 156..205  
id R06283  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(408..446)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 33..71

id R06283  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 328..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 286..342  
id AA152388  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 89..141  
id AA152388  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 242..283  
id AA152388  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..85
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 1..44  
id AA152388  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 351..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 312..367  
id AA159107  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 408..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 371..403  
id AA159107  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..225
- (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 93  
region 166..198  
id AA159107  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(171..324)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 313..466  
id AA152366  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(328..406)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 232..310  
id AA152366  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(408..446)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 190..228  
id AA152366  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 39..80  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq FLTALLWRGRIPG/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

|                                                                   |             |
|-------------------------------------------------------------------|-------------|
| AGCGGAGACG CAGAGTCTTG AGCAGCGCGN CAGGCACC ATG TTC CTG ACT GCG CTC | 56          |
| Met Phe Leu Thr Ala Leu                                           | -10         |
| CTC TGG CGC GGC CGC ATT CCC GGC CGT CAG TGG ATC GGG AAG CAC CGG   | 104         |
| Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg   | -5 1 5      |
| CSG CCG CGG TTC GTG TCG TTG CGC GCC AAG CAG AAC ATG ATC CGC CGC   | 152         |
| Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg   | 10 15 20    |
| CTG GAG ATC GAG GCG GAG AAC CAT TAC TGG CTG AGC ATG CCC TAC ATG   | 200         |
| Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met   | 25 30 35 40 |
| ACC CGG GAG CAG GAG CGC GGC CAC GCC SSG TTG CGC AGG AGG GAG GCC   | 248         |
| Thr Arg Glu Gln Glu Arg Gly His Ala Xaa Leu Arg Arg Arg Glu Ala   | 45 50 55    |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTC GAG GCS ATA AAG GCG GCC GCC ACT TCC AAG TTC CCC CCG CAT AGA | 296 |
| Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg |     |
| 60 65 70                                                        |     |
|                                                                 |     |
| TTC ATT GCG GAC CAG CTC GAC CAT CTC AVK VGT CAC CAA GAA ATG GTC | 344 |
| Phe Ile Ala Asp Gln Leu Asp His Leu Xaa Xaa His Gln Glu Met Val |     |
| 75 80 85                                                        |     |
|                                                                 |     |
| CTA ATC CTG AGT CGT CAC CCT TGG ATT TTA TGG ATC ACG GAG CTG ACC | 392 |
| Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr |     |
| 90 95 100                                                       |     |
|                                                                 |     |
| ATC TTT ACC TGG TCT GGA CTG AAA AAC TGT AGC TTG TGT GAA AAT GAG | 440 |
| Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu |     |
| 105 110 115 120                                                 |     |
|                                                                 |     |
| CTT TGG ACC AGT CTT TAT                                         | 458 |
| Leu Trp Thr Ser Leu Tyr                                         |     |
| 125                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..391  
id W56872  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..291  
id W31727  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..375
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..354  
id W16469  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..400  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..356  
id N31028  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 22..375  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..354  
id W16470  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 120..389  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.3  
seq TCLTACWTALCCC/CL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AACTTGCTCT GAGACAGGTG CGGCAAGTCT ACTGCGGGCT GGTCCGGGCT CCTCAGGTTC | 60  |
| AGACCCGACC GTTATCCAGT CGGTTTCGTGG AGAGGAGAGG TGSACTTTAC AGGTCCCCG | 119 |
| ATG AAC CAA GAG AAC CCT CCA CCA TAT CCA GGC CCT GGT CCA ACG GCC   | 167 |
| Met Asn Gln Glu Asn Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala       |     |
| -90 -85 -80 -75                                                   |     |
| CCA TAC CCA CCT TAT CCA CCA CAA CCA ATG GGT CCA GGA CHT ATG GGG   | 215 |
| Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly   |     |
| -70 -65 -60                                                       |     |
| GGA CCC TAC CCA CCT CCT CAA GGG TAC CCC TAC CAA GGA TAC CCA CAG   | 263 |
| Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln   |     |
| -55 -50 -45                                                       |     |
| TAC GGC TGG CAG GGT GGA CCT CAG GAG CCT CCT AAA ACC ACA GTG TAT   | 311 |
| Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr   |     |
| -40 -35 -30                                                       |     |
| GTG GTA GAA GAC CAA AGA AGA GAT GAG CTA GGA CCA TCC ACC TGC CTC   | 359 |
| Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu   |     |
| -25 -20 -15                                                       |     |
| ACA GCC TGC TGG ACG GCT CTC TGT TGC TGC TGT CTC TGG               | 398 |
| Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp               |     |
| -10 -5 1                                                          |     |

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 56..332  
id AA022276  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 4..59  
id AA022276  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 329..368  
id AA022276  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..284
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 44..273  
id W87295  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 274..321  
id W87295  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..47  
id W87295  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 318..357  
id W87295  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..264  
id W01758  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 261..300  
id W01758  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 50..249  
id W57829  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 3..49  
id W57829  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..214  
id HUM417E03B

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 11..172
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq LIVWLLVKSFSSES/GI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

AAGTTCGCC ATG GCC TCC TTG GAA GTC AGT CGT AGT CCT CGC AGG TCT 49
 Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser
 -50 -45

CGG CGG GAG CTG GAA GTG CGC AGT CCA CGA CAG AAC AAA CAT TCG GTG 97
Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val
 -40 -35 -30

CTT TTA CCT ACC TAC AAC GAG CGC GAR GAA CTG CCG CTC ATC GTG TGG 145
Leu Leu Pro Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp
 -25 -20 -15 -10

CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA ATT ATA 193
Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile
 -5 1 5

ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT GAA CAG 241
Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln
 10 15 20

TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA CGA GAG 289
Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu
 25 30 35

AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CAT GGA ATG RAA ACA TGC 337
Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys
 40 45 50 55

CAC AGG RAA CTA CAT CAT TAT TAT GGA TGC 367
His Arg Xaa Leu His His Tyr Tyr Gly Cys
 60 65

```

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 61..399  
id AA114853  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 11..60  
id AA114853  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..391  
id W23545  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 42..381  
id AA069652  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..41  
id AA069652  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 8..333  
id AA084987  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..347  
id AA101916  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 303..344
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq CPTCLCAPSXXWG/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

```
ATCCGGTGCA CGCGAGTSTT CTGAAACGTC AGCTGCGCTC CCCTAGGAGT GCTGAGCCCCG 60
CGGAACCGCA GCCATGACTG AGGCTGATGT GAATCCAAAG GYCTATCCCC TTGCCGATGC 120
CCACCTCACC AAGAAGCTAC TGGACCTCGT TCAGCAGTCA TGTA ACTATA AGCAGCTTCG 180
GAAAGGWGCC AATGAGGCCA CCAA AACCT CAACAGGGGC ATCTCTGAGT TCATCGTGAT 240
GGCTGCAGAC GCCGAGCCAC TGGAGATCAT TCTGCACCTG CCGCTGCTGT GTGAAGACAA 300
GA ATG TGC CCT ACG TGT TTG TGC GCT CCA AGC AVN SCC TGG GGA GAG 347
 Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu
 -10 -5 1

CCT GTG GGG TCT CCA GGC CTG TCA TCG CCT GTT CTG TCA CCA TCA AAG 395
Pro Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys
 5 10 15

AAG GCT CGC AGC
Lys Ala Arg Ser
 20

 407
```

## (2) INFORMATION FOR SEQ ID NO: 252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 34..159  
id N52621  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..38



(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..31  
id N52621  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..168  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 5..152  
id AA157163  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..66  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq AVAASAASGQAEG/KK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

```
ACTTCTAAG ATG GCT GCC GCT ACC GGT GCG GTG GCA GCC TCG GCC GCC TCG 51
Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser
 -15 -10

GGT CAG GCG GAA GGT AAA AAG ATC ACC GAT CTG CGG GTC ATC GAT CTG 99
Gly Gln Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu
-5 1 5 10

AAG TCC GAG CTG AAG CGG CGG AAC TTA GAC ATC ACC GGA GTC AAG ACC 147
Lys Ser Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr
 15 20 25

GTG CTC ATC TCC CGA CTA AGG 168
Val Leu Ile Ser Arg Leu Arg
 30
```

## (2) INFORMATION FOR SEQ ID NO: 253:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 132..343

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 95..306  
id AA102280  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 37..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..103  
id AA102280  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 340..433  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 304..397  
id AA102280  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 132..433  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 87..388  
id R13711  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 71..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 27..95  
id R13711  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 132..401  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 87..356  
id R61022  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 71..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 27..95  
id R61022  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 132..389  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 82..339  
                           id N44705  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 50..139  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..90  
                           id N44705  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 387..433  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 338..384  
                           id N44705  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 126..433  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 75..382  
                           id H29689  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 23..73  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.2  
                           seq SLLXRVSVTAVAA/LS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ATTCCTCCTG CCCGTAGTAG CC ATG GCG GCC ATG AGT TTG TTG CKG CGG GTT | 52  |
| Met Ala Ala Met Ser Leu Leu Xaa Arg Val                          |     |
| -15 -10                                                          |     |
| TCG GTT ACT GCG GTG GCA GCT CTG TCT GGC CGG CCC CTT GGC ACY NGC  | 100 |
| Ser Val Thr Ala Val Ala Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa  |     |
| -5 1 5                                                           |     |
| CTC GGA TTT GGG GGC TTC CTC ACT CGT GGC TTT CCG AAG GCT GCT GCT  | 148 |
| Leu Gly Phe Gly Gly Phe Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala  |     |
| 10 15 20 25                                                      |     |
| CCT GTT CGA CAC AGT GGA GAC CAT GGG AAA AGA CTA TTT GTC ATC AGA  | 196 |
| Pro Val Arg His Ser Gly Asp His Gly Lys Arg Leu Phe Val Ile Arg  |     |
| 30 35 40                                                         |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CCT TCT AGA TTC TAT GAC AGG CGT TTT TTG AAG TTA TTG AGA TTC TAC | 244 |
| Pro Ser Arg Phe Tyr Asp Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr |     |
| 45 50 55                                                        |     |
|                                                                 |     |
| ATT GCA TTG ACT GGG ATT CCA GTA GCA WTT TTC ATA ACT CTG GTG AAT | 292 |
| Ile Ala Leu Thr Gly Ile Pro Val Ala Xaa Phe Ile Thr Leu Val Asn |     |
| 60 65 70                                                        |     |
|                                                                 |     |
| GTA TTC ATT GGT CAA GCT GAA CTA GCA GAA ATT CCA GAA GGC TAT GTC | 340 |
| Val Phe Ile Gly Gln Ala Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val |     |
| 75 80 85                                                        |     |
|                                                                 |     |
| CCA GAA CAC TGG GAA TAT TAT AAG CAT CCC ATA TCA AGA TGG ATT GCC | 388 |
| Pro Glu His Trp Glu Tyr Tyr Lys His Pro Ile Ser Arg Trp Ile Ala |     |
| 90 95 100 105                                                   |     |
|                                                                 |     |
| CGT AAT TTC TAT GAT AGT CCT GMA AAG ATA TAT GAA AGA ACA ATG     | 433 |
| Arg Asn Phe Tyr Asp Ser Pro Xaa Lys Ile Tyr Glu Arg Thr Met     |     |
| 110 115 120                                                     |     |

## (2) INFORMATION FOR SEQ ID NO: 254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..452
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 43..409  
id W00599  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 12..54  
id W00599  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 107..404  
id AA088577

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 29..96  
id AA088577  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..41
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 1..36  
id AA088577  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..189
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..156  
id R18030  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 156..279  
id R18030  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 46..207  
id H85485  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 61..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LDLLRGLPRVSLA/NL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

GAGACCACGT GGCCTCCGAG CA3CTCAGGG CGCCCTTGAA AGTTCTTGGA TCTGCGGGTT 60

ATG GCC GGT CCC TTG CAG GGC GGT GGG GCC CGG GCC CTG GAC CTA CTC 108  
Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu

| -25                                                             | -20                                                             | -15 | -10 |    |
|-----------------------------------------------------------------|-----------------------------------------------------------------|-----|-----|----|
| CGG GGC CTG CCG CGT GTG AGC CTG GCC AAC TTA AAG CCG AAT CCC GGC | Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly | 156 |     |    |
|                                                                 | -5                                                              | 1   | 5   |    |
| TCC AAG AAA CCG GAG AGA AGA CCA AGA GGT CGG AGA AGA GGT AGA AAA | Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Arg Gly Arg Lys | 204 |     |    |
|                                                                 | 10                                                              | 15  | 20  |    |
| TGT GGC AGA GGC CAT AAA GGA GAA AGG CAA AGA GGA ACC CGG CCC CGC | Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg | 252 |     |    |
|                                                                 | 25                                                              | 30  | 35  |    |
| TTG GGC TTT GAG GGA GGC CAG ACT CCA TTT TAC ATC CGA RTC CCA AAA | Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys | 300 |     |    |
|                                                                 | 40                                                              | 45  | 50  | 55 |
| TAC GGG TTT AAC GAA GGA CAT AGT TTC AGA CGC CAG TAT AAG CCT TTG | Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu | 348 |     |    |
|                                                                 | 60                                                              | 65  | 70  |    |
| AGT CTC AAT AGA CTG CAG TAT CTT ATT GAT TTG GGT CGT GTT GAT CCT | Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro | 396 |     |    |
|                                                                 | 75                                                              | 80  | 85  |    |
| AGT CAA CCT ATT GAC TTA ACC CAG CTT GTC AAT GGG AGA GGT GTG ACC | Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr | 444 |     |    |
|                                                                 | 90                                                              | 95  | 100 |    |
| ATC GCG CCG                                                     | Ile Ala Pro                                                     | 453 |     |    |
|                                                                 | 105                                                             |     |     |    |

## (2) INFORMATION FOR SEQ ID NO: 255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..103  
id T11164  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 133..223  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 102..192  
 id T11164  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 18..140  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.1  
 seq GILILWIIRLLFS/KT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAGGAAGCG GCTAACT ATG GCG ACC GCC ACG GAG CAG TGG GTT CTG GTG  | 50  |
| Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val                     |     |
| -40 -35                                                         |     |
| GAG ATG GTA CAG GCG CTT TAC GAG GCT CCT GCT TAC CAT CTT ATT TTG | 98  |
| Glu Met Val Gln Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu |     |
| -30 -25 -20 -15                                                 |     |
| GAA GGG ATT CTG ATC CTC TGG ATA ATC AGA CTT CTT TTC TCT AAG ACT | 146 |
| Glu Gly Ile Leu Ile Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr |     |
| -10 -5 1                                                        |     |
| TAC AAA TTA CAA GAA CGA TCT GAT CTT ACA GTC AAG GAA AAA GAA GAA | 194 |
| Tyr Lys Leu Gln Glu Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu |     |
| 5 10 15                                                         |     |
| CTG ATT GAA GAG TGG CAA CCA GAA CCT CTT GTT CCT CCT GTC CCA AAA | 242 |
| Leu Ile Glu Glu Trp Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys |     |
| 20 25 30                                                        |     |
| GAC CAT CCT GCT CTC AAC TAC AAC ATC GTT TCA GGC CCT CCA AGC CAC | 290 |
| Asp His Pro Ala Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His |     |
| 35 40 45 50                                                     |     |
| AAA ACT GTG GTG AAT GGA AAA GAA TGT ATA AAC TTC GCC TCA TTT AAT | 338 |
| Lys Thr Val Val Asn Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn |     |
| 55 60 65                                                        |     |
| TTT CTT GGA TTG TTG GAT AAC CCT AGG GTT AAG GCA GCA GCT TTA GCA | 386 |
| Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala |     |
| 70 75 80                                                        |     |
| TCT CTA AAG AAG TAT GGC GTG GGG ACT TGT GGA CCC TGT             | 425 |
| Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys             |     |
| 85 90 95                                                        |     |

## (2) INFORMATION FOR SEQ ID NO: 256:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 base pairs  
 (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 124..305  
id W16517  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..123  
id W16517  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 302..361  
id W16517  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 10..144  
id H23328  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 145..274  
id H23328  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 276..309
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 275..308  
id H23328



est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 147..309  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 146..308  
id H06320  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 73..149  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 69..145  
id H06320  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 5..40  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..36  
id H06320  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 146..182  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 222..258  
id T62768  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 162..398  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq QGVLFICFTCARS/FP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```
AAAACTGAG GCCTGGGAGC AGGAACCTGT AGGCAGCGCT TGAGGGTAGC GGGATAGCAG 60
CTGCAACGCG CGTGGGAGGC GGGGGCTCTG GCGGAACAA AAATCACAGG ATGTCAGAGG 120
ATGTTTCCCG GGAAGAACTG GGATAAAGGG GTCCCAGCAC C ATG GAG GAC CCG AAC 176
 Met Glu Asp Pro Asn
 -75

CCT GAA GAG AAC ATG ADG CAG CAG GAT TCA CCC AAG GAG AGA AGT CCC 224
Pro Glu Glu Asn Met Xaa Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro
 -70 -60

CAG ASC CCA GGA GGC AAC ATC TGC CAC CTG GGG GCC CCG AAG TGC ACC 272
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Pro | Gly | Gly | Asn | Ile | Cys | His | Leu | Gly | Ala | Pro | Lys | Cys | Thr |     |
|     |     |     | -55 |     |     |     |     | -50 |     |     |     |     | -45 |     |     |     |
| CGC | TGC | CTC | ATC | ACC | TTC | GCA | GAT | TCC | AAG | TTS | SAG | GAG | CGT | CAC | ATG | 320 |
| Arg | Cys | Leu | Ile | Thr | Phe | Ala | Asp | Ser | Lys | Xaa | Xaa | Glu | Arg | His | Met |     |
|     |     | -40 |     |     |     |     | -35 |     |     |     |     | -30 |     |     |     |     |
| AAG | CGG | GAG | CAC | CCA | GCG | GAC | TTC | GTG | GCC | CAG | AAG | CTG | CAG | GGG | GTC | 368 |
| Lys | Arg | Glu | His | Pro | Ala | Asp | Phe | Val | Ala | Gln | Lys | Leu | Gln | Gly | Val |     |
|     | -25 |     |     |     |     | -20 |     |     |     |     | -15 |     |     |     |     |     |
| CTC | TTC | ATC | TGC | TTC | ACC | TGC | GCC | CGC | TCC | TTC | CCC | TCT |     |     |     | 407 |
| Leu | Phe | Ile | Cys | Phe | Thr | Cys | Ala | Arg | Ser | Phe | Pro | Ser |     |     |     |     |
| -10 |     |     |     |     | -5  |     |     |     |     | 1   |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(166..452)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 16..302  
id AA062591  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..45  
id AA158358  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 444..490
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 43..89  
id AA158358  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..45  
id AA158431  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 444..490  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 43..89  
id AA158431  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 65..160  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq RLLSSLLLTMSNN/NP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```
AAGGATCCTC TACCGGCTTT TCGAGTCAGT GCTGCCGCCG CTGCCCGCGG CTTTGCAGAG 60
CAGG ATG AAT GTG ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG 109
 Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu
 -30 -25 -20

CAC TCC AAC GTG CGG CTC CTC AGC AGC TTG TTA CTT ACA ATG AGT AAT 157
His Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn
 -15 -10 -5

AAC AAC CCT GAG TTA TTC TCC CCA CCT CAG AAG TAC CAG CTT TTG GTG 205
Asn Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val
 1 5 10 15

TAT CAT GCA GAT TCT CTC TTT CAT GAT AAG GAA TAT CGG AAT GCT GTG 253
Tyr His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val
 20 25 30

AGT AAG TAT ACC ATG GCT TTA CAG CAG AAG AAA GCG CTA AGT AAA ACT 301
Ser Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr
 35 40 45

TCA AAA GTG AGA CCT TCA ACT GGA AAT TCT GCA TCT ACT CCA CAA AGT 349
Ser Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser
 50 55 60

CAG TGT CTT CCA TCT GAA ATT GAA GTG AAA TAC AAA ATG GCT GAA TGT 397
Gln Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys
 65 70 75

TAT ACA ATG CTA AAA CAA GAT AAA GAT GCC ATT GCT ATA CTT GAT GGG 445
Tyr Thr Met Leu Lys Gln Asp Lys Asp Ala Ile Ala Ile Leu Asp Gly
 80 85 90 95

KST CCC TTC AAG ACA AAG AAC TCC CAR AAT AAA CAT GAT GCT GGC 490
Xaa Pro Phe Lys Thr Lys Asn Ser Gln Asn Lys His Asp Ala Gly
```

## (2) INFORMATION FOR SEQ ID NO: 258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..312  
id HSC26F061  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 20..260  
id W30546  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 66..252  
id H34739  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 125..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq LVHHCPTWQWATG/EE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
AGGGTGCTGC CWKCCGGGTG CTGWTGCGAG TCGGTGGCAG CGAGGACATT TTCTGACTCC 60
CTGGCCCCTG ACACGGCTGC ACTTTCCATC CCGTCGCGGG GCCGGCCGCT ACTCCGGCCC 120
CAGG ATG CAG AAT GTG ATT AAT ACT GTG AAG GGA AAG GCA CTG GAA GTG 169
Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val
```

-55

-50

-45

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GCT GAG TAC CTG ACC CCG GTC CTC AAG GAA TCA AAG TTT AAG GAA ACA | 217 |
| Ala Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr |     |
| -40 -35 -30                                                     |     |
|                                                                 |     |
| GGT GTA ATT ACC CCA GAA GAG TTT GTG GCA GCT GGA GAT CAC CTA GTC | 265 |
| Gly Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val |     |
| -25 -20 -15                                                     |     |
|                                                                 |     |
| CAC CAC TGT CCA ACA TGG CAA TGG GCT ACA GGG GAA GAA TTG AAA GTG | 313 |
| His His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val |     |
| -10 -5 1 5                                                      |     |
|                                                                 |     |
| AAG GCA TAC CTA CCA ACA GGC AAA TGG                             | 340 |
| Lys Ala Tyr Leu Pro Thr Gly Lys Trp                             |     |
| 10                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 259:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 89..262  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..428
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 334..402  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 260..321  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 40..88  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..69
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..44  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 428..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 401..438  
id W68068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 62..285  
id AA083574  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..43  
id AA083574  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 401..444  
id AA083574  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 314..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 312..345  
id AA083574

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 283..313  
id AA083574  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 102..264  
id AA001460  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 336..441  
id AA001460  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 262..323  
id AA001460  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 28..79  
id AA001460  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 78..254  
id H72445  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 252..313  
id H72445  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 66..113  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 32..79  
id H72445  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 34..69  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..36  
id H72445  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 382..411  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 349..378  
id H72445  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 209..472  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq CIQRLPWLLLCRG/IT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```
AGATCCCGCC TGGGGCCGGC TGAGTGGCAC TTAAGCGGGC CATGCCATGC AACCTGGGGC 60
GCTGCCAACC GTGGGCGAGC TCTGGGTGTG CGGGCGGCCT GGCGCGGCGC TCCGCTGTGT 120
CAGCGTGTTA TGATGCCGTC CCGTACCAAC CTGGCTACTG GAATCCCCAG TAGTAAAGTS 180
AAATATTCAA GGCTCTCCAG CACAGACG ATG GCT ACA TTG ACC TTC AGT TTA 232
 Met Ala Thr Leu Thr Phe Ser Leu
 -85

AGA AAA CCC CTC CAA AGA TCC CTT ATA AGG CCA TCG CAC TTG CCA CTG 280
Arg Lys Pro Leu Gln Arg Ser Leu Ile Arg Pro Ser His Leu Pro Leu
-80 -75 -70 -65

TGC TGT TTT GAT TGG CGC CTT TCT CAT TAT TAT AGG CTC CCT CCT GCT 328
Cys Cys Phe Asp Trp Arg Leu Ser His Tyr Tyr Arg Leu Pro Pro Ala
 -60 -55 -50

GTC AGG CTA CAT CAG CAA AGG GGG GGC AGA CCG GGC CGT TCC AGT GCT 376
Val Arg Leu His Gln Gln Arg Gly Gly Arg Pro Gly Arg Ser Ser Ala
```



|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| -45                                                             | -40 | -35 |     |
| GAT CAT TGG CAT TCT GGT GTT CCT ACC CGG ATT TTA CCA CCT GCG CAT |     |     | 424 |
| Asp His Trp His Ser Gly Val Pro Thr Arg Ile Leu Pro Pro Ala His |     |     |     |
| -30                                                             | -25 | -20 |     |
| CGC TTA CTA TGC ATC CAA AGG CTA CCG TGG TTA CTC CTA TGC AGG GGG |     |     | 472 |
| Arg Leu Leu Cys Ile Gln Arg Leu Pro Trp Leu Leu Leu Cys Arg Gly |     |     |     |
| -15                                                             | -10 | -5  |     |
| ATC ACT AGT                                                     |     |     | 481 |
| Ile Thr Ser                                                     |     |     |     |
| 1                                                               |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 67..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 51..202  
id N55991  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..59  
id N55991  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..231
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..143  
id R57473  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 232..339
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 143..250  
id R57473  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..243  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 195..298  
id H79944  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 243..279  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 299..335  
id H79944  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..237  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 97..194  
id H70394  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 235..325  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 193..233  
id H70394  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..325  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 80..265  
id W31972  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 123..269  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq PSLAAGLLFGSXA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AAATCGCGTT TCCSGAGAGA CCTGGCTGCT GTGTCCCGCG GCTTGCCTC CGTAGTGGAC 60

```

TCCGCGGGGCC TTCGGCAGAT GCAGGCCTGG GGTAGTCTCC TTTCTGGACT GAGAAGAGAA 120

GA ATG GAG AAG CCC CTC TTC CCA TTA GTG CCT TTG CAT TGG TTT GGC 167
Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly
 -45 -40 -35

TTT GGC TAC ACA GCA CTG GTT GTT TCT GGT GGG ATC GTT GGC TAT GTA 215
Phe Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val
 -30 -25 -20

AAA ACA GGC AGC GTG CCG TCC CTG GCT GCA GGG CTG CTC TTC GGC AGT 263
Lys Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
 -15 -10 -5

VWA GCC GGC CTG GGT GCT TAC CAG CTG TAT CAG GAT CCA AGR AAC GTT 311
Xaa Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val
 1 5 10

TGG GGT TTC CTA GCC GCT ACA TCT GTT 338
Trp Gly Phe Leu Ala Ala Thr Ser Val
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 261:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 92..238  
id R27748  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..89  
id R27748  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 162..298
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 116..252  
id T79527  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..47  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 11..56  
id T79527  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..90  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 61..98  
id T79527  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 95..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 59..159  
id R08734  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 194..241  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 159..206  
id R08734  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..90  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 14..56  
id R08734  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 102..298  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 32..228  
id H35655  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 102..298  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: .identity 90  
region 108..304  
id AA038389  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 108..161  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq VAVGLTIAAAGFA/GR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```
AGGGGGTTGC GTCGCTCTCT GGTAAGGCG TGCAGGTGTT GGCCGCGGCC TCTGAGCTGG 60
GATGAGCCGT GCTCCCGGTG GAAGCAAGGG GAGCCCCAGC SGGAGCC ATG GCC AGT 116
 Met Ala Ser
ACA GTG GTA GCA GTT GGA CTG ACC ATT GCT GCT GCA GGA TTT GCA GGC 164
Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly
-15 -10 -5 1
CGT TAC GTT TTG CAA GCC ATG AAG CAT ATG GAG CBT CAA GTA AAA CAA 212
Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Xaa Gln Val Lys Gln
 5 10 15
GTT TTT CAA AGC CTA CCA AAA TCT GCC TTC AGT GGT GGC TAT TAT AGA 260
Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg
 20 25 30
GGT BGG TTT GAA CCC ARA ATG RCA AAA CGG GAA GCA GCG GGG 302
Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala Gly
 35 40 45
```

## (2) INFORMATION FOR SEQ ID NO: 262:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..311  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 96..277  
id T32007

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..98  
id T32007  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 76..260  
id R19207  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..78  
id R19207  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 76..260  
id R36562  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..78  
id R36562  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 76..260  
id R59039  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 19..78  
id R59039  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..314  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 70..254  
id T35666  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 59..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..72  
id T35666  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 136..384  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq AFSFSRLLSQCRP/DC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```
AAAGTTCTCC TTCCACCTTC CCCCACCCTT CTCTGCCAAC CGCTGTTTCA GCCCCTAGCT 60
GGATTCCAGC CATTGCTGCA GCTGCTCCAC AGCCCTTTTC AGGACCCAAA CAACCGCAGC 120
CGCTGTTCCC CAGGR ATG GTG ATC CGT GTA TAT ATT GCA TCT TCC TCT GGC 171
 Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
 -80 -75

TCT ACA GCG ATT AAG AAG AAA CAA CAA GAT GTG CTT GGT TTC CTA GAA 219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
-70 -65 -60

GCC AAC AAA ATA GGA TTT GAA GAA AAA GAT ATT GCA GCC AAT GAA GAG 267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
-55 -50 -45 -40

AAT CGG AAG TGG ATG AGA GAA AAT GTA CCT GAA AAT AGT CGA CCA GCG 315
Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala
-35 -30 -25

GTT CAG GGG CCA CAT GCT TTT CGG TAT AAA GCA TTC TCC TTC TCT AGG 363
Val Gln Gly Pro His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg
-20 -15 -10

TTG CTA TCA CAG TGC AGA CCT GAC TGC CTG AAT ATG CTC AGG AGA TTT 411
Leu Leu Ser Gln Cys Arg Pro Asp Cys Leu Asn Met Leu Arg Arg Phe
-5 1 5

AGT CAA TAT TGT CTG TAT TTG GTT ATG GAA AAG GCT CTC CTT TTT TTT 459
```

Ser Gln Tyr Cys Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe  
10 15 20 25

TTT TTT  
Phe Phe

465

## (2) INFORMATION FOR SEQ ID NO: 263:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 117..274  
id R14800  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..116  
id R14800  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 315..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 302..355  
id R14800  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 270..302  
id R14800  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..330



(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 113..311  
id R59757  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 54..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 36..112  
id R59757  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 18..58  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..41  
id R59757  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 132..330  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 94..292  
id R25047  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 54..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 17..93  
id R25047  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 59..352  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 38..331  
id R23993  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 163..294  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 163..294  
id W23811  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 132..194  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 131..193  
                           id W23811  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 305..354  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 308..357  
                           id W23811  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 350..390  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 354..394  
                           id W23811  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 243..368  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4  
                           seq ITSSLFLGRGSA/SN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AAGAAGCCGG TGGCCGCGCA GGAGGACGGA GCCCTAACCG CAACCCGCGC CGCGCCGCGC 60
CGATTTGATT TGTATCCACT GTCACCAGCA CTGCTCACTT AGGACTTTCT GGATCCAGAC 120
CCAGGCAGCG CACACTGGAC TCTTGAGGAA GAAGGAGACT CTAATTTTGG ATTCCTTGGT 180
GGAGGAAAAT AAAACACTCT GGTCTTGCCG CCAACGATGC AAGTGTGACT GCTGGCGTCT 240
TC ATG AGC TCC AGA GGT CAC AGC ACG CTA CCA AGG ACT CTC ATG GCC 287
 Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala
 -40 -35 -30

CCT CGG ATG ATT TCC GAG GGA GAC ATA GGA GGC ATT GCT CAA ATC ACC 335
Pro Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr
 -25 -20 -15

TCC TCT CTA TTC CTG GGC AGA GGC AGT GTG GCC TCC AAT CGG CAC CTC 383
Ser Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu
 -10 -5 1 5

CTC CAG GCT CGT GGC ATC 401
Leu Gln Ala Arg Gly Ile
 10

```

## (2) INFORMATION FOR SEQ ID NO: 264:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..183  
id AA022583  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(69..228)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 281..440  
id AA022584  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 66..119
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq PALCLFDVDGTLT/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```
AGGAAGTTCC GGGCCGAGTT CCTCGTGCCA ACGTGTCTTG TAAGGTGCGG CTAGAAACTG 60
GGGAC ATG GCA GCG CCT GGC CCA GCG CTC TGC CTC TTC GAC GTG GAT GGG 110
 Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly
 -15 -10 -5
ACC CTC ACC GCC CCG CGG CAG AAA ATT ACC AAA GAA ATG GAT GAC TTC 158
Thr Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe
 1 5 10
CTA CAA AAA TTG AGG CAG AAG ATC AAA ATC GGA GTG GTA GGC GGA TCG 206
Leu Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser
 15 20 25
GAC TTT GAG AAA GTG CAG GAA CGG 230
Asp Phe Glu Lys Val Gln Glu Arg
 30 35
```

## (2) INFORMATION FOR SEQ ID NO: 265:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 159..278  
id H97758  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 107..160  
id H97758  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 166..250  
id N59486  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 114..167  
id N59486  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 148..201  
id R09724  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..51  
id R09724  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 200..229  
id R09724  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..178
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 170..247  
id W90369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 121..171  
id W90369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 240..285  
id W90369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..90  
id N56221  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 126..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq ILFHGVFYAGGFA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
ACTGGAAGAA CTCGTCATGC TCTTTGTAGC GTGGTGCTTC TGTTGCTCAC AGGACAACTT 60
GCCTTTGATG ATTTTCAAGA GAGTTGTGCT ATGATGTGGC AAAGTATGCA GGAAGCAGGC 120
GGTCA ATG CCT CTG GGA GCA AGG ATC CTT TTC CAC GGT GTG TTC TAT GCC 170
 Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
 -15 -10 -5

GGG GGC TTT GCC ATT GTG TAT TAC CTC ATT CAA AAG TTT CAT TCC AGG 218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
 1 5 10

ACA CTG
Thr Leu 224
```

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..216  
id HUM429E03B  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 235..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 211..303  
id HUM429E03B  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 107..310  
id T80259  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 15..114  
id T80259  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..245  
id T31768  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 271..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 234..290  
id T31768  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 47..272  
id N32697  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..97
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..43  
id N32697  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..263  
id N44613  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 156..194
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq MLLSIGMLMLSAT/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

GCCTAGGTGT TGTCGTCCCT GCTAGTACTC CGGGCTGTGG GGGTCGGTGC GGATATTCAG 60
TCATGAAATC AGGGTAGGGA CTTCTCCCGC AGCGACGCGG CTGGCAAGAC TGTTTGTGTT 120
GCGGGGGCCG GACTTCAAGG TGATTTTACA ACGAG ATG CTG CTC TCC ATA GGG 173
 Met Leu Leu Ser Ile Gly
 -10
ATG CTC ATG CTG TCA GCC ACA CAA GTC TAC ACC ATC TTG ACT GTC CAG 221
Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr Ile Leu Thr Val Gln
 -5 1 5
CTC TTT GCA TTC TTA AAC CTA CTG CCT GTA GAA GYA GAC ATT TTA GCA 269
Leu Phe Ala Phe Leu Asn Leu Leu Pro Val Glu Xaa Asp Ile Leu Ala
 10 15 20 25
TAT AAC TTT GAA AAT GCA TCT CAG ACA TTT GAT GAC CTC CCT GCA AGA 317
Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp Asp Leu Pro Ala Arg
 30 35 40
TTT GGT TAT
Phe Gly Tyr 326

```

(2) INFORMATION FOR SEQ ID NO: 267:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..368  
id AA150637  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 30..294  
id H02768  
est

## (ix) FEATURE:



(A) NAME/KEY: other  
(B) LOCATION: 181..372  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 148..339  
id H70139  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 33..179  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..147  
id H70139  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(267..394)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 231..358  
id W46236  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(184..277)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 349..442  
id W46236  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(109..164)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 464..519  
id W46236  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 188..366  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 72..250  
id N30922  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 117..180  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..64  
id N30922  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 111..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq WIAAVTIAAGTAA/IG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

AATCGCGGAG TCGGTGCTTT AGTACGCCGC TGGCACCTTT ACTCTCGCCG GCCGCGCGAA 60
CCC GTTTGAG CTCGGTATCC TAGTGACACAC GCCTTGCAAG CGACGGCGCC ATG AGT 116
 Met Ser
 -25

CTG ACT TCC AGT TCC AGC GTA CGA GTT GAA TGG ATC GCA GCA GTT ACC 164
Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr
 -20 -15 -10

ATT GCT GCT GGG ACA GCT GCA ATT GGT TAT CTA GCT TAC AAA AGA TTT 212
Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe
 -5 1 5

TAT GTT AAA GAT CAT CGA AAT AAA GCT ATG ATA AAC CTT CAC ATC CAG 260
Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln
 10 15 20 25

AAA GAC AAC CCC AAG ATA GTA CAT GCT TTT GAC ATG GAG GAT TTS RNA 308
Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Xaa Xaa
 30 35 40

GAT AAA GCT GTG TAC TGC CGT TGT TGG AGG TCC AAA AAG TTC CCA TTC 356
Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe
 45 50 55

TGT GAT GGG GCT CAC ACA ARM VAT AAC GAA GAG ACT GGG CTG 398
Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu
 60 65 70

```

## (2) INFORMATION FOR SEQ ID NO: 268:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..150
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 31..126  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 151..212  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 126..187  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 24..58  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..35  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 211..242  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 185..216  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 55..263  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 202..410  
id R54574  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 24..58  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 172..206  
id R54574  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 55..176  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 159..280  
id R13710  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 174..235  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 279..340  
id R13710  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 24..58  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 129..163  
id R13710  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 55..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 189..299  
id T78111  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 163..203  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 298..338  
id T78111  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 24..58  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 159..193  
id T78111  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 201..235  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 337..371  
id T78111  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 70..252  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq YTAVSVLGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```

AATTACGCAG AGAGAAAGTT ACGAGAAACT CGTTTTTCATC TTCTTGGTTT CATCYTAAAT 60
ACCAACGTC ATG TCT GGT TCT AAT GGT TCC AAA GAA AAT TCT CAC AAT AAG 111
 Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys
 -60 -55 -50

GCT CGG ACG TCT CCT TAC CCA GGT TCA AAA GTT GAA CGA AGC CAG GTT 159
Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val
 -45 -40 -35

CCT AAT GAG AAA GTG GGC TGG CTT GTT GAG TGG CAA GAC TAT AAG CCT 207
Pro Asn Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro
 -30 -25 -20

GTG GAA TAC ACT GCA GTC TCT GTC TTG GCT GGA CCC AGG TGG GCA GAT 255
Val Glu Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp
 -15 -10 -5 1

CCT CAG ATC AGT GAV AGT VAT TTT TCT CCC AAG TTT AAC GAA AAG GAT 303
Pro Gln Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp
 5 10 15

GGG CAT GTT GAG AGA NAG AGC AAG AAT GGC CTG TAT GAG ATT GAN AAT 351
Gly His Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn
 20 25 30

GGA AGA CCG AGA AAT CCT GCA GAC GGA CTG GAC TGG TGG GCC 393
Gly Arg Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala
 35 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 269:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 137..335  
id HSC1QH021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 126..263  
id HUML12288  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 25..111  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..87  
id HUML12288  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 178..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..266  
id R60742  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 154..303  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 133..232  
id HSC07D011  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..147  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 35..129  
id HSC07D011  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 18..49  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..32  
id HSC07D011  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 154..298  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 136..230  
id C04685  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 25..147

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 10..132  
id C04685  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 349..438  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq LWMRWTVTSTTRA/WI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```
AAAACCTTAG CAAGATGGCG GCTCCCTGGG CGTCCCTGCG CCTGGTCGCC CCCATGTGGA 60
ATGGGCGTAT CAGGGGCATC CATCGCCTGG GTGCGGCAGT GGCCCCAGAG GGCAATCAGA 120
AGAAGAAAAG GACAATAMTC CARPTYCCTG GMCCVAASTA TTTCTACGAT GTGGAGGCTC 180
TGAGGGATTA CTTGCTCCAA AGGGAGATGT ACAAGGTGCA TGAGAAAAAT CGATCTTACA 240
CCTGGCTGGA GAAGCAACAT GGTCCATACG GCGCAGGTGC CTTTTTCATC CTGAAGCAGG 300
GAGGCGCAGT CAAGTTTCGA GACAAGGAGT GGATCAGGCC AGATAAGT ATG GCC ATT 357
 Met Ala Ile
 -30

TCT CTC AGG AGT TCT GGA ATT TCT GTG AAG TGC CTG TCG AAG CTG TGG 405
Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser Lys Leu Trp
 -25 -20 -15

ATG CGG TGG ACT GTG ACA TCA ACT ACG AGG GCC TGG ATM RNN GCN GAA 453
Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile Xaa Ala Glu
 -10 -5 1 5

CCT CCG CAG CTG GAC ATC TCG 474
Pro Pro Gln Leu Asp Ile Ser
 10
```

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Uterus

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 82..210

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 49..177  
id AA082886  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 47..83  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 15..51  
id AA082886  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 17..97  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq FVLGSARLGGSGS/MR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AACATTAACC GGCAGG ATG TCG GAG GTG CGG CTG CCA CCG CTA CGC GCC CTG | 52  |
| Met Ser Glu Val Arg Leu Pro Pro Leu Arg Ala Leu                   |     |
| -25 -20                                                           |     |
| GAC GAC TTT GTT CTG GGG TCG GCG CGT CTT GGC GGC TCC GGA TCC ATG   | 100 |
| Asp Asp Phe Val Leu Gly Ser Ala Arg Leu Gly Gly Ser Gly Ser Met   |     |
| -15 -10 -5 1                                                      |     |
| CGA CCC GCT GCG ATG GTG YHA CCG CGT CAT CAA CAA CCT CCT CTA CTA   | 148 |
| Arg Pro Ala Ala Met Val Xaa Pro Arg His Gln Gln Pro Pro Leu Leu   |     |
| 5 10 15                                                           |     |
| CCA AAC CAA CTA CCT TCT CTG CTT CGG CAT CGG CCT CGC TCT CGC CGG   | 196 |
| Pro Asn Gln Leu Pro Ser Leu Leu Arg His Arg Pro Arg Ser Arg Arg   |     |
| 20 25 30                                                          |     |
| GTA CGT ACG GCC ACG                                               | 211 |
| Val Arg Thr Ala Thr                                               |     |
| 35                                                                |     |

## (2) INFORMATION FOR SEQ ID NO: 271:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle



## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 177..257  
id W93162  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 107..177  
id W93162  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 174..254  
id W67415  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..112
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 52..102  
id W67415  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 132..174  
id W67415  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 174..254  
id N44655  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 104..174  
id N44655

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 41..170  
id HSBA7H051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 170..226  
id HSBA7H051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..40  
id HSBA7H051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 63..169  
id R37538  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 169..249  
id R37538  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..39  
id R37538  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 206..250
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq LVSATAWLEECWW/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```
AGGCGGCGAA GATGGCGGAG AACAGCGGTC GCGCCGGCAA GAGCAGCGGG AGCGNCGCGN 60
GGAAGGGGGC GGTGTCCGCA GAGCAGGTGA TTGCTGGCTT CAACCGCCTT CGGCAGGAAC 120
AGCGAGGCCT GGCATCCAAA GCAGCTGAGT TGGAGATGGA GTTGAATGAG CACAGCCTAG 180
TGAATCGATA CACTGAAGGA GGTAG ATG AAA CTC GTA AGT GCT ACC GCA TGG 232
 Met Lys Leu Val Ser Ala Thr Ala Trp
 -15 -10

TTG GAG GAR TGC TGG TGG AGC GAA CTG TCA 262
Leu Glu Glu Cys Trp Trp Ser Glu Leu Ser
-5 1
```

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 142..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 120..360  
id HUML1108  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 17..127  
id HUML1108  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 37..395  
id AA156844  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 137..500  
id HSU51712  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 237..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 112..270  
id T70871  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 9..111  
id T70871  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 105..213  
id H48308  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 177..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 206..315  
id H48308  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 314..347  
id H48308  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 309..410
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.3  
seq LYPVLLAVCCLES/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

AAGCTTCCAA ACCCAGGGCT TGCCTTGCC TTTGCCTCTT CCACCGCGCA GGGACCATGT 60  
CGGCGGAGAC CGCGAGCGGC CCCACAGAGG ACCAGGTGGA AATCCTGGAG TACAACTTCA 120  
ACAAGGTCGA CAAGCACCCG GATTCCACCA CGCTGTGCCT CATCGCGGCC GAGGCAGGCC 180  
TTTCCGAGGA GGAGACCCAG AAATGGTTTA AGCAGCGCCT GGCAAAGTGG CGGCGCTCAG 240  
AAGGCCTGCC CTCAGAGTGC AGATCCGTCA CAGACTAAGG AGATGGCAGG CATTGACAGC 300  
TTCCTCC ATG AAG GCC ATC TCT GTT TCT CTC CTC CGC TTA ACC AAG CTG 350  
Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu  
-30 -25  
TTG TGG TTT TTC AGC ATA GTG TTG TAT GTT CCA TTG CTA GCT GTC TGC 398  
Leu Trp Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys  
-20 -15 -10 -5  
TGT TTA CAC AGT GTT GTA TTT TTT 422  
Cys Leu His Ser Val Val Phe Phe  
1

## (2) INFORMATION FOR SEQ ID NO: 273:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..421
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 179..405  
id AA010986  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..91  
id AA010986  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..205  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 91..188  
id AA010986  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 443..505  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 429..491  
id AA010986  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 417..449  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 402..434  
id AA010986  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..205  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..187  
id W96112  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 316..494  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 300..478  
id W96112  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 195..336  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 178..319  
id W96112  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 69..513  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..445  
id W44481  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 2..193  
id AA129812  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 184..289  
id AA129812  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 340..396  
id AA129812  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 301..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 291..342  
id AA129812  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 405..448
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 397..440  
id AA129812  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..289  
id W40172  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..439
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 343..440

id W40172  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 285..342  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 285..342  
id W40172  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 85..438  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq LMIALTUVVGCIFM/VI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTCCAACGC TGGGTGACAT TGAGCTCACC AGCGCCACCG TCCCCGGCGA AGTTCTGCGC | 60  |
| TGGTCGGCGG AGTASCAAGT GGCC ATG GGG AGC CTC AGC GGT CTG CGC CTG    | 111 |
| Met Gly Ser Leu Ser Gly Leu Arg Leu                               |     |
| -115 -110                                                         |     |
| GCA GCA GGA AGC TGT TTT AGG TTA TGT GAA AGA GAT GTT TCC TGN TCT   | 159 |
| Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val Ser Xaa Ser   |     |
| -105 -100 -95                                                     |     |
| CTA AGG CTT ACC AGA AGC TCT GAT TTA AAG AGA ATA AAT GGA TTT TGC   | 207 |
| Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn Gly Phe Cys   |     |
| -90 -85 -80                                                       |     |
| ACA AAA CCA CAG GAA AGT CCC GGA GCT CCA TCC CGC ACT TAC AAC AGA   | 255 |
| Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr Tyr Asn Arg   |     |
| -75 -70 -65                                                       |     |
| GTG CCT TTA CAC AAA CCT ACG GAT TGG CAG AAA AAG ATC CTC ATA TGG   | 303 |
| Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile Leu Ile Trp   |     |
| -60 -55 -50                                                       |     |
| TCA GGT CGC TTC AAA AAG GAA ANB NAA ATC CCA GAG ACT CTC TCG TTG   | 351 |
| Ser Gly Arg Phe Lys Lys Glu Xaa Xaa Ile Pro Glu Thr Val Ser Leu   |     |
| -45 -40 -35 -30                                                   |     |
| GAG ATG CTT GAN STT GCA AAG AAC AAG ATG CGA GTG AAG ATC AGC TAT   | 399 |
| Glu Met Leu Xaa Xaa Ala Lys Asn Lys Met Arg Val Lys Ile Ser Tyr   |     |
| -25 -20 -15                                                       |     |
| CTA ATG ATT GCC CTG ACG GTG GTA GGA TGC ATC TTC ATG GTT ATT GAG   | 447 |
| Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met Val Ile Glu   |     |
| -10 -5 1                                                          |     |
| GGC AAG AAG GCT GCC CAA AGA CAC GAG ACT TTA ACA AGC TTG MAC TTA   | 495 |
| Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser Leu Xaa Leu   |     |
| 5 10 15                                                           |     |
| GAA AAG AAA GCT CGT CTG                                           | 513 |



Glu Lys Lys Ala Arg Leu  
20 25

## (2) INFORMATION FOR SEQ ID NO: 274:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 190..399  
id AA001815  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 35..141  
id AA001815  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 139..198  
id AA001815  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 139..341  
id N42162  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 2..147

id N42162  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 144..300  
id N24414  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 10..95  
id N24414  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 93..152  
id N24414  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 122..338  
id W76137  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..73  
id W76137  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 71..130  
id W76137  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..360
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 121..283  
id H03817  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 77..147  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..72  
id H03817  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 346..402  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 270..326  
id H03817  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 146..205  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 70..129  
id H03817  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..358  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq LASSFLFTMGGLG/FI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

|                                                                 |            |            |            |            |          |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|----------|----|
| ACTGTTTNGG                                                      | GGAGGCGCGT | GGGGCTTGAG | GCCGAGAACG | GCCCTTGCTG | CCACCAAC | 58 |
| ATG GAG ACT TTG TAC CGT GTC CCG TTC TTA GTG CTC GAA TGT CCC AAC | 106        |            |            |            |          |    |
| Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn |            |            |            |            |          |    |
| -100 -95 -90 -85                                                |            |            |            |            |          |    |
| CTG AAG CTG AAG AAG CCG CCC TGG TTG CAC ATG CCG TCG GCC ATG ACT | 154        |            |            |            |          |    |
| Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr |            |            |            |            |          |    |
| -80 -75 -70                                                     |            |            |            |            |          |    |
| GTG TAT GCT CTG GTG GTG GTG TCT TAC TTC CTC ATT ACC GGA GGA ATA | 202        |            |            |            |          |    |
| Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile |            |            |            |            |          |    |
| -65 -60 -55                                                     |            |            |            |            |          |    |
| ATT TAT GAT GTT ATT GTT GAA CCT CCA AGT GTC GGT TCT ATG ACT GAT | 250        |            |            |            |          |    |
| Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp |            |            |            |            |          |    |
| -50 -45 -40                                                     |            |            |            |            |          |    |
| GAA CAT GGG CAT CAG AGG CCA GTA GCT TTC TTG GCC TAC AGA GTA AAT | 298        |            |            |            |          |    |

Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn  
 -35 -30 -25

GGA CAA TAT ATT ATG GAA GGA CTT GCA TCC AGC TTC CTA TTT ACA ATG 346  
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met  
 -20 -15 -10 -5

GGA GGT TTA GGT TTC ATA ATC CTG GAC GGA TCG RNT GCA CCA AAT ATC 394  
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Xaa Ala Pro Asn Ile  
 1 5 10

CCA AAA CTC AAT AGA TTC 412  
 Pro Lys Leu Asn Arg Phe  
 15

## (2) INFORMATION FOR SEQ ID NO: 275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
 region 80..182  
 id C05215  
 est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 73..111
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
 seq MLVLRSGLTALA/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

CACTCGGGAA GACTTCAGAG AAGTCTCACA AAGGACTCGG CTGGGTGCTT TTCTCAGTGC 60

CGAAGCCGCG CC ATG CTC GTT CTC AGA AGC GGC CTG ACC AAG GCG CTT GCC 111  
 Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala  
 -10 -5

TCA CGG ACG CTC GCG CVT CAG AKA AWT TTT GCT CAT CGA GCT GAA GTT 159  
 Ser Arg Thr Leu Ala Xaa Gln Xaa Xaa Phe Ala His Arg Ala Glu Val  
 1 5 10 15

CGG AAA GCC TTA GCC AAC TGT AAG GAA TGG CAA GAA CAA TCT ATC ATT 207

Arg Lys Ala Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile  
20 25 30  
CCA AAT TTG GCT CGC ATT GAT AAA CAA GAG ACC AGG 243  
Pro Asn Leu Ala Arg Ile Asp Lys Gln Glu Thr Arg  
35 40

## (2) INFORMATION FOR SEQ ID NO: 276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 77..206  
id R87832  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 1..77  
id R87832  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 65..194  
id HUM427G10B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..65  
id HUM427G10B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 112..241  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 52..181  
                           id R52722  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 62..113  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 1..52  
                           id R52722  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 111..241  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 79..209  
                           id W41484  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 30..137  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
                           seq NIESLAWTGGTLG/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

|             |             |           |     |     |     |     |     |     |     |     |     |
|-------------|-------------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAGTTTCCTG  | CGAGCTCGGC  | TTCCTCAAC | ATG | GCT | GCG | CCC | TTG | TCA | GTG | GAG | 53  |
|             | Met         | Ala       | Ala | Pro | Leu | Ser | Val | Glu |     |     |     |
|             | -35         |           |     |     |     |     | -30 |     |     |     |     |
| GTG GAG TTC | GGA GGT GGT | GCG GAS   | TCC | TGT | TTG | ACG | GTA | TTA | AGA | AAC | 101 |
| Val Glu Phe | Gly Gly Ala | Xaa Ser   | Cys | Leu | Thr | Val | Leu | Arg | Asn |     |     |
|             | -25         |           | -20 |     |     |     | -15 |     |     |     |     |
| ATC GAG TCA | CTT GCC TGG | ACA GGA   | GGA | ACC | CTG | GGA | CAT | CCG | GAA | CCT | 149 |
| Ile Glu Ser | Leu Ala Trp | Thr Gly   | Gly | Thr | Leu | Gly | His | Pro | Glu | Pro |     |
|             | -10         |           | -5  |     |     |     | 1   |     |     |     |     |
| GCT CAT CTG | GAT CAA GAA | GAA TTT   | GCT | AAA | AGA | GCG | GCC | ASA | GTT | GTT | 197 |
| Ala His Leu | Asp Gln Glu | Glu Phe   | Ala | Lys | Arg | Ala | Ala | Xaa | Val | Val |     |
| 5           |             | 10        |     | 15  |     |     | 20  |     |     |     |     |
| CAT CCA GGG | AGA CAG CGT | GCG GCC   | AGG | AAT | TCT | GGT | GCT | GAC | TAC | AGG | 245 |
| His Pro Gly | Arg Gln Arg | Ala Ala   | Arg | Asn | Ser | Gly | Ala | Asp | Tyr | Arg |     |
|             | 25          |           | 30  |     |     |     | 35  |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 277:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..382  
id AA127626  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 44..329  
id W39584  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 330..384  
id W39584  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..60
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 3..39  
id W39584  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(47..403)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 68..424  
id N32838  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(56..403)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 67..414

id AA121528  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 164..378  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 130..344  
id AA082078  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 36..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..130  
id AA082078  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 198..392  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq FVGGLPVIFWSWA/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```

ACTTAGTCGT GTGTACATCA TTGGGAATGG AGGGAAATAA ATGACTGGAT GGTCGCTGCT 60
TTTTAAGTTT CAAATTGACA TTCCAGACAA GCGGTGCCTG AGCCTGTGCC TGTCTTCAGA 120
TCTTCACAGC ACAGTTCCTG GGAAGGTGGA GCCACCAGCC TCTCCTTGAA TAACTGGGAG 180
ATGAPACAGG AAGCTCT ATG ACA CAC TTG ATC GAA TAT GAC AGA CAC CGA 230
 Met Thr His Leu Ile Glu Tyr Asp Arg His Arg
 -65 -60 -55

AAA TCA CGA CTC AGC CCC CTC CAG CAC CTC TAC CTG TTG CCC GCC GAT 278
Lys Ser Arg Leu Ser Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp
 -50 -45 -40

CAC AGC CGG AAT GCA GCT GAA AGA TTC CCT GGG GCC TGG TTC CAA CCG 326
His Ser Arg Asn Ala Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro
 -35 -30 -25

CCC ACT GTG GAC TCT GAG GCC TCT GCA TTT GTG GGT GGT CTG CCT GTG 374
Pro Thr Val Asp Ser Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val
 -20 -15 -10

ATA TTT TGG TCA TGG GCT GGT CTG GTC 401
Ile Phe Trp Ser Trp Ala Gly Leu Val
 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 278:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 335 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Uterus
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 70..337  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 1..268  
                            id HSC2SG081  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 71..251  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 1..181  
                            id R13964  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 256..334  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 100  
                            region 184..262  
                            id R13964  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 26..255  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 94  
                            region 1..230  
                            id HUML13589  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 116..251  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 1..136  
                            id H05572  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 256..337  
    (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 139..220  
id H05572  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 24..89  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq WARKLLSVPWLLC/GP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AACAGTTACG CGCCGCACGG ATC ATG GCC GCA GCC GCT CTG GGG CAG ATC TGG 53  
Met Ala Ala Ala Ala Leu Gly Gln Ile Trp  
-20 -15

GCA CGA AAG CTT CTC TCT GTC CCT TGG CTT CTG TGT GGT CCC AGA AGA 101  
Ala Arg Lys Leu Leu Ser Val Pro Trp Leu Leu Cys Gly Pro Arg Arg  
-10 -5 1

TAT GCC TCC TCC AGT TTC AAG GCT GCA GAC CTG CAG CTG GAA ATG ACA 149  
Tyr Ala Ser Ser Ser Phe Lys Ala Ala Asp Leu Gln Leu Glu Met Thr  
5 10 15 20

CAG AAG CCT CAT AAG AAG CCT GGC CCC GGC GAG CCC CTG GTG TTT GGG 197  
Gln Lys Pro His Lys Lys Pro Gly Pro Gly Glu Pro Leu Val Phe Gly  
25 30 35

AAG ACA TTT ACC GAC CAC ATG CTG ATG GTG GAA TGG AAT GAC AAG GGC 245  
Lys Thr Phe Thr Asp His Met Leu Met Val Glu Trp Asn Asp Lys Gly  
40 45 50

TGG GGC CAG CCC CGA ATC CAG CCC TTC CAG AAC CTC ACG CTG CAC CCA 293  
Trp Gly Gln Pro Arg Ile Gln Pro Phe Gln Asn Leu Thr Leu His Pro  
55 60 65

GCC TCC TCC AGC CTC CAC TAC TCC CTG CAG CTG TTT GAG GGC 335  
Ala Ser Ser Ser Leu His Tyr Ser Leu Gln Leu Phe Glu Gly  
70 75 80

## (2) INFORMATION FOR SEQ ID NO: 279:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 57..176  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 50..169  
id AA126817  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 219..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 213..338  
id AA126817  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 10..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 2..336  
id W79731  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..326  
id H21245  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 31..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 34..305  
id H11314  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 302..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 306..348  
id H11314  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 41..202  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 22..183  
id W19587  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 201..284  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 183..266  
 id W19587  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 283..344  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 266..327  
 id W19587  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 48..161  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq CPLLLLVTNNG/RH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```

AAGGGGTCGG AGGTCAGGGC GAGCGTCTCG CAGGCCGTAG GAGGAAG ATG GCG GTG 56
 Met Ala Val

GAG TCG CGC GTT ACC CAG GAG GAA ATT AAG AAG GAG CCA GAG AAA CCG 104
Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro Glu Lys Pro
-35 -25 -20

ATC GAC CGC GAG AAG ACA TGC CCA CTG TTG CTA CTG GTC TTC ACC ACC 152
Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu Leu Val Phe Thr Thr
-15 -10 -5

AAT AAC GGC CGC CAC CAC CGA ATG GAC GAG TTC TCC CGG GGA AAT GTA 200
Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg Gly Asn Val
 1 5 10

CCG TCC AGC GAG TTG CAG ATC TAC ACT TGG ATG GAT GCA ACT TTG AAA 248
Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala Thr Leu Lys
 15 20 25

GAA CTG ACA AGC TTA GTA AAA GAA GTC TAC CCA GAA GCT AGA WAG AAG 296
Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala Arg Xaa Lys
 30 35 40 45

GGC ACT CAC TTC AAT TTT GCA VTC GTT TTT ACA GAT GTT AAA AGA CCT 344
Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val Lys Arg Pro
 50 55 60

```

## (2) INFORMATION FOR SEQ ID NO: 280:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 72..338  
id W79829  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 332..363  
id W79829  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 14..280  
id H62624  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 274..305  
id H62624  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 24..290  
id H81957  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 59..324  
id W82998  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 111..376  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 64..329  
id AA023811  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 240..305  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq AVLDCAFYDPTHA/WS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
ACTAGCCTGC GAGTGTCTCTG AGGGAAGCAA GGAGGCGGCG GCGGCCGCAG CGAGTGGCGA 60
GTAGTGGAAA CGTTGCTTCT GAGGGGTGTC CAAGATGASC GGTTCKAMCG GAGKTCAAGC 120
TGAACCAGCC ACCCGAGGAT GGCATCTCCT CCGTGAAGTT CAGCCCCAAC ACCTCCCACT 180
TCCTGCTTGT CTCCTCCTGG GACACGTCCG TCGTCTCTTA CGATGTGCCG GCCAACTCC 239
ATG CGG CTC AAG TAC CAG CAC ACC GGC GCC GTC CTG GAC TGC GCC TTC 287
Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 -20 -15 -10

TAC GAT CCA ACG CAT GCC TGG AGT GGA GGA CTA GAT CAT CAA TTG AAA 335
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
 -5 1 5 10

ATG CAT GAT TTG AAC ACT GAT CAA GAA AAT CTT GTT GGG ACC ATG ATG 383
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
 15 20 25

CCC CTA TCA GAT GTG TTG 401
Pro Leu Ser Asp Val Leu
 30
```

## (2) INFORMATION FOR SEQ ID NO: 281:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 87..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 72..257  
id T60345  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 47..89  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 33..75  
id T60345  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 14..47  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..34  
id T60345  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 87..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 75..260  
id T46853  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 12..89  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..78  
id T46853  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 87..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 39..159  
id R57601  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92

region 144..223  
id R57601  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..89  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..42  
id R57601  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 84..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 55..166  
id W71083  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 12..269  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq WAVVLADTAVTSG/RG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATAGGCGCAA | G   | ATG | GCG | CTG | CTT | TTT | GCA | CGT | TCT | TTG | CGC | TTG | TGC | CGC | 50  |     |
|            | Met | Ala | Leu | Leu | Phe | Ala | Arg | Ser | Leu | Arg | Leu | Cys | Arg |     |     |     |
|            | -85 |     |     |     |     |     | -80 |     |     |     |     | -75 |     |     |     |     |
| TGG        | GGA | GCC | AAA | CGA | TTG | GGA | GTT | GCC | TCC | ACA | GAG | GCC | CAG | AGA | GGC | 98  |
| Trp        | Gly | Ala | Lys | Arg | Leu | Gly | Val | Ala | Ser | Thr | Glu | Ala | Gln | Arg | Gly |     |
|            | -70 |     |     |     |     |     | -65 |     |     |     |     | -60 |     |     |     |     |
| GTC        | AGT | TTC | AAA | CTG | GMA | GAA | AAA | ACC | GCC | CAC | AGC | AGC | CTG | GCA | CTC | 146 |
| Val        | Ser | Phe | Lys | Leu | Xaa | Glu | Lys | Thr | Ala | His | Ser | Ser | Leu | Ala | Leu |     |
|            | -55 |     |     |     |     |     | -50 |     |     |     |     | -45 |     |     |     |     |
| TTC        | AGA | GAT | GAT | ACG | GGT | GTC | AAA | TAT | GGC | TTG | GTG | GGA | TTG | GAG | CCC | 194 |
| Phe        | Arg | Asp | Asp | Thr | Gly | Val | Lys | Tyr | Gly | Leu | Val | Gly | Leu | Glu | Pro |     |
|            | -40 |     |     |     |     |     | -35 |     |     |     |     | -30 |     |     |     |     |
| ACC        | AAG | GTG | GCC | TTG | AAT | GTG | GAG | CGC | TTC | CGG | GAG | TGG | GCA | GTG | GTG | 242 |
| Thr        | Lys | Val | Ala | Leu | Asn | Val | Glu | Arg | Phe | Arg | Glu | Trp | Ala | Val | Val |     |
|            | -25 |     |     |     |     | -20 |     |     |     | -15 |     |     |     | -10 |     |     |
| CTG        | GCA | GAC | ACA | GCG | GTC | ACC | AGT | GGC | AGA | GGG |     |     |     |     |     | 275 |
| Leu        | Ala | Asp | Thr | Ala | Val | Thr | Ser | Gly | Arg | Gly |     |     |     |     |     |     |
|            |     |     |     | -5  |     |     |     |     |     | 1   |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 282:

## (1) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE.
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 77..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq ILLGNYCVAVADA/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```

ATTCCCCCTT GGGCGGTGGT GGAGGTGGTA ACCGTGATAG TAGCAGCTCC GGCGGCAGCA 60
ACAGCGACTA CGAGGG ATG GCG GCG GCT GCA GCA GGA ACT SNA ACA TCC CAG 112
 Met Ala Ala Ala Ala Ala Gly Thr Xaa Thr Ser Gln
 -65 -60

AGG TTT TTC CAG AGC TTC TCG GAT GCC CTA ATC GAC GAG GAC CCC CAG 160
Arg Phe Phe Gln Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln
 -55 -50 -45

GCG GCG TTA GAG GAG CTG ACT AAG GCT TTG GAA CAG AAA CCA GAT GAT 208
Ala Ala Leu Glu Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp
 -40 -35 -30 -25

GCA CAG TAT TAT TGT CAA AGA GCT TAT TGT CAC ATT CTT CTT GGG AAT 256
Ala Gln Tyr Tyr Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn
 -20 -15 -10

TAC TGT GTT GCT GTT GCT GAT GCA AAG AAG TCT CTA GAA CTC AAT CCA 304
Tyr Cys Val Ala Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro
 -5 1 5

AAT AAT TCC ACT GCT ATG CTG AGA AAA GGA ATA TGT GAA TAC CAT GAA 352
Asn Asn Ser Thr Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu
 10 15 20

AAA AAC TAT GCT GCT GCC CTA GAA ACT TTT TAC AGA AGG ACG GGG 397
Lys Asn Tyr Ala Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly
 25 30 35

```

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 79..380  
id H17763  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 4..55  
id H17763  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 96..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 82..363  
id H16532  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..53  
id H16532  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..370
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 46..337  
id R52491  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 65..247  
id R21494  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..53  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..52  
id R21494  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 266..305  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 268..307  
id R21494  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 129..321  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 71..263  
id AA084554  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 315..379  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 256..320  
id AA084554  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 139..318  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq WFYIGSSLNGTRG/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```
AGTGGCCCCG ATGTTCCGGTG CAGCTGCCAG ATCCGCTGAT CTAGTGCTTC TCGAAAAAAA 60
CCTTCAGGGG GCCCATGGCT GTCGATATTC AACCAGCATG CCTTGGACTT TATTSYGGGA 120
AGACCCTATT ATTTAAAA ATG GCT CAA CTG AAA TAT ATG GAG AAT GTG GGG 171
 Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly
 -60 -55 -50
TAT GCC CAA GAG GAC AGA GAA CGA ATG CAC AGA AAT ATT GTC AGC CTT 219
Tyr Ala Gln Glu Asp Arg Glu Arg Met His Arg Asn Ile Val Ser Leu
 -45 -40 -35
GCA CAG AAT CTC CTG AAC TTT ATG ATT GGC TCT ATC TTG GAT TTA TGG 267
Ala Gln Asn Leu Leu Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp
 -30 -25 -20
```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAA TGC TTC CTC TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG | 315 |
| Gln Cys Phe Leu Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg |     |
| -15 -10 -5                                                      |     |
|                                                                 |     |
| GGA AAA AGA GTT CCA GCG CAC TTT TCC AAC ACA TCA CTG CAT TAT TTG | 363 |
| Gly Lys Arg Val Pro Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu |     |
| 1 5 10 15                                                       |     |
|                                                                 |     |
| AAT GCA GCA TGG CCG CGG                                         | 381 |
| Asn Ala Ala Trp Pro Arg                                         |     |
| 20                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..294
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..292  
id HUM524F05B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 48..176  
id H81799  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 170..279  
id H81799  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..43
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 16..50  
id H81799  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..172  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 57..181  
id T84779  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 167..226  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 175..234  
id T84779  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 1..45  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 7..51  
id T84779  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 167..294  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 101..228  
id W81213  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 66..172  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..107  
id W81213  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 8..172  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..165  
id AA090080  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 167..210

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 159..202  
id AA090080  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 174..266  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq WSPLSTRSGGTHA/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```
AAAAACAATA GGACGGAAAC GCCGAGGAAC CCGGCTGAGG CGGCAGAGCA TCCTGGCCAG 60
AACAAGCCAA GGAGCCAAGA CGAGAGGGAC ACACGGACAA ACAACAGACA GAAGACGTAC 120
TGGCCGCTGG ACTCCKCTGC CTCCCCATC TCCCCGCCAT CTGCGCCCGG AGG ATG 176
 Met
AGC CCA GCC TTC AGG GCC ATG GAT GTG GAG CCC CGC GCC AAA GGS TCC 224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30 -25 -20 -15

TTC TGG AGC CCT TTG TCC ACC AGG TCG GGG GGC ACT CAT GCG TGC TCC 272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
 -10 -5 1

GCT TCA ATG AGA CAA CCC TGG 293
Ala Ser Met Arg Gln Pro Trp
 5
```

## (2) INFORMATION FOR SEQ ID NO: 285:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 26..326  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 42..342  
id R71425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..345  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 11..337  
id AA133412  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(114..345)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 172..403  
id AA156940  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(71..114)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 402..445  
id AA156940  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(26..76)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 439..489  
id AA156940  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 172..345  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 186..359  
id W07240  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..171  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 83..182  
id W07240  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..76  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 33..88  
id W07240  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..307  
id R81019  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 18..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq SILAQVLDQSARA/RL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

AGCGCTGACG CCGAGCC ATG GCG GAC GAG GAG CTT GAG GCG CTG AGG AGA 50
 Met Ala Asp Glu Leu Glu Ala Leu Arg Arg
 -50 -45

CAG AGG CTG GCC GAG CTG CAG GCC AAA CAC GGG GAT CCT GGT GAT GCG 93
Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala
 -40 -35 -30

GCC CAA CAG GAA GCA AAG CAC AGG GAA GCA GAA ATG AGA AAC AGT ATC 146
Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile
 -25 -20 -15

TTA GCC CAA GTT CTG GAT CAG TCG GCC CGG GCC AGG TTA AGT AAC TTA 194
Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu
 -10 -5 1 5

GCA CTT GTA AAG CCT GAA AAA ACT AAA GCA GTA GAG AAT TAC CTT ATA 242
Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile
 10 15 20

CAG ATG GCA AGA TAT GGA CAA CTA AGT GAG AAG GTA TCA GAA CAA GGT 290
Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly
 25 30 35

TTA ATA GAR ATC CTT AAA AAA GTA AGC CAA CAA ACA GAA AAG AHN ACA 338
Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys Xaa Thr
 40 45 50

ACA GTG AGG
Thr Val Arg
 55

```

347

## (2) INFORMATION FOR SEQ ID NO: 286:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 186..382

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 156..352  
id AA082259  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 61..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 34..119  
id AA082259  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 29..61

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 1..33  
id AA082259  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 194..331

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 169..306  
id H80945  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 54..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 30..122  
id H80945  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 157..345

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5  
seq GLVCAGLADMARPAE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

AACAGCGGGC AGGGAAAGCC GCGGGAAGGG TACTCCAGGC GAGAGGCGGA CGCGAGTCGT 60
CGTGGCAGGA AAAGTGACTA GCTCCCCTTC GTTGTACAGCC AGGGACGAGA ACACAGCCAC 120
GCTCCCAMCC GGCTGCCHAA GRWTCCTTSG GCGGCG ATG TCG GCC GCC GGT GCC 174
 Met Ser Ala Ala Gly Ala
 -60
CGA GGC CTG CGG GCC ACC TAC CAC CGG CTC CTC GAT AAA GTG GAG CTG 222
Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
-55 -50 -45
ATG CTG CCC GAG AAA TTG AGG CCG TTG TAC AAC CAT CCA GCA GGT CCC 270
Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
-40 -35 -30
AGA ACA GTT TTC TTC TGG GCT CCA ATT ATG AAA TGG GGG TTG GTG TGT 318
Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
-25 -20 -15 -10
GCT GGA TTG GCT GAT ATG GCC AGA CCT GCA GAA AAA CTT AGC ACA GCT 366
Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
-5 1 5
CAA TCT GVK GTT TTG ATG GCT ACA GGG TTT ATT TGG TCA AGA TAC TCG 414
Gln Ser Xaa Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser
10 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 287:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 196..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 185..380  
id W07314  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..204
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 46..192  
id W07314

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 409..478
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 401..470  
id W07314  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 12..390  
id W07582  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..393
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 31..379  
id W73850  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..37  
id W73850  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..447
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..375  
id AA112776  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..388
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..326  
id H72671  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 98..355
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5

seq TGXLNMTLQRASA/AP

(xi) SEQUENCE DESCRIPTION: SEQ.ID NO: 287:

AACTTGTCTAG CCCTTGTCTG AGGCGGAGGC AGCCCCGCGC CGCGCCGGAC CCGAGCATAT 60

TTCATTTTCT GTCATTGGAC TTTGAGCCAT TAGAACC ATG AGC AAC TAC AGT GTG 115  
Met Ser Asn Tyr Ser Val  
-85

TCA CTG GTT GGC CCA GCT CCT TGG GGT TTC CGG CTG CAG GGC GGT AAG 163  
Ser Leu Val Gly Pro Ala Pro Trp Gly Phe Arg Leu Gln Gly Gly Lys  
-80 -75 -70 -65

GAT TTC AAC ATG CCT CTG ACA ATC TCT AGT CTA AAA GAT GGC GGC AAG 211  
Asp Phe Asn Met Pro Leu Thr Ile Ser Ser Leu Lys Asp Gly Gly Lys  
-60 -55 -50

GCA GCC CAG GCA AAT GTA AGA ATA GGC GAT GTG GTT CTC AGC ATT GAT 259  
Ala Ala Gln Ala Asn Val Arg Ile Gly Asp Val Val Leu Ser Ile Asp  
-45 -40 -35

GGA ATA AAT GCA CAA GGA ATG ACT CAT CTT GAA GCC CAG AAT AAG ATT 307  
Gly Ile Asn Ala Gln Gly Met Thr His Leu Glu Ala Gln Asn Lys Ile  
-30 -25 -20

AAG GGT TGT ACA GGA NYT TTG AAT ATG ACT CTG CAA AGA GCA TCT GCT 355  
Lys Gly Cys Thr Gly Xaa Leu Asn Met Thr Leu Gln Arg Ala Ser Ala  
-15 -10 -5

GCA CCC AAG CCT GAG CCG GTT CCT GTT CAA AAG CCC ACA GTC ACC AGC 403  
Ala Pro Lys Pro Glu Pro Val Pro Val Gln Lys Pro Thr Val Thr Ser  
1 5 10 15

GTG TGT TCC GAG ACT TCT CAG GAG CTA GCA GAG GGA CAG AGA AGA GGA 451  
Val Cys Ser Glu Thr Ser Gln Glu Leu Ala Glu Gly Gln Arg Arg Gly  
20 25 30

TCC CAG GGT GAC AGT AAA CAG CAA AAT 478  
Ser Gln Gly Asp Ser Lys Gln Gln Asn  
35 40

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 4..333  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..330  
id N35568  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 26..297  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..272  
id R35915  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 295..338  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 271..314  
id R35915  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..255  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..212  
id W31312  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..355  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 209..313  
id W31312  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 13..320  
id HSC1MA011  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 62..339  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..278  
id R61491  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 245..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LLGLELSEAEAIG/AD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

ATTCGTTTAC AGTTCGGCAC GTAGGACGGA GGGTAGTGCG TCTAGAGACA CATATTCCCA 60
ACGGATTTGA CGATGGTGTT CGGTCTTGAA TGGAAATGTA GTCTTAGGCC AGTCTTAGGT 120
TTTTGAACAG GATAGTAGGT ATCCGGAGTC GATTGAGGGC CAGAGCAGGC ACTGGGGTTC 180
GGATCCTGGG CAAAGTTTCC CACATTGAGG GTCTCGAGGA CGCCTAGATC TCTTTCCCAG 240
GGCC ATG GCG AAC CCG AAG CTG CTG GGA CTG GAG CTA AGC GAG GCG GAG 289
 Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
 -15 -10 -5

GCG ATC GGT GCT GAT TCG GCG CGA TTT GAG GAG CTG CTG CTG CAG GCC 337
Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
 1 5 10

TCG AAG GAG CTC CAG CAA
Ser Lys Glu Leu Gln Gln
 15

```

## (2) INFORMATION FOR SEQ ID NO: 289:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 90..178  
id W21193  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 2..53  
id W21198  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 71..111  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 49..89  
id W21198  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(114..201)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 271..358  
id AA061731  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(114..201)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 271..358  
id AA061768  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(125..201)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 269..345  
id AA058174  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 204..323  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq ALLCTLLLHFQNI/RR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```
AAAGGTGTCT GGATCGGAGG GAGGTTCTGGG TGGGCATCGG GCGGCTGGAA GAGCTCGACT 60
CGTCCCGCTG GGAAAGCGCG AGTCTGAGTG GAACCCTGGA CGACTTGCAG AGCGGCTGGC 120
GCACTCATGG CGGACTACTG GAAGTCACAG CCAAAGAAAT TCTGTGATTA CTGCAAGTGC 180
TGGATAGCAG ACAATAGGCC TGT ATG ATA ATT CCG CTG TTA GAG ATT CTA ATA 233
 Met Ile Ile Pro Leu Leu Glu Ile Leu Ile
 -40 -35
ATA ATT TTG TTG AAT GAA GTG CTC CTT TTT GAT GTA AAC TCA GTT TAC 281
```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Ile Ile Val Leu Asn Glu Val Leu Leu Phe Asp Val Asn Ser Val Tyr |     |
| -30 -25 -20 -15                                                 |     |
| AAA GCA CTT TTA TGT ACA TTG CTC TTG CAT TTT CAA AAC ATC AGA AGA | 329 |
| Lys Ala Leu Leu Cys Thr Leu Leu Leu His Phe Gln Asn Ile Arg Arg |     |
| -10 -5 1                                                        |     |
| TTT CTG TCT TCT CAG TCC CCT ATG AAA GCT GTG AGC CTT CTA THT TTT | 377 |
| Phe Leu Ser Ser Gln Ser Pro Met Lys Ala Val Ser Leu Leu Xaa Phe |     |
| 5 10 15                                                         |     |
| CAT CAA CCT GAC TTT GAT TAT ATA                                 | 401 |
| His Gln Pro Asp Phe Asp Tyr Ile                                 |     |
| 20 25                                                           |     |

## (2) INFORMATION FOR SEQ ID NO: 290:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..382
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 97  
region 4..337  
id HUMGPCRB  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..54  
id T29782  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 345..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 55..92  
id T29782  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 80..235



(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.4  
 seq LVFIIGLVGNLLA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AACTTCAGTT TGGACAACTA CTCACAGCTA CTACACAGAG ACCCGAACGA GTCAGTGATA 60
TACACCTGGA CCACCACCA ATG GAT ATA CAA ATG GCA AAC AAT TTT ACT CCG 112
 Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro
 -50 -45

CCC TCT GCA ACT CCT CAG GGA AAT GAC TGT GAC CTC TAT GCA CAT CAC 160
Pro Ser Ala Thr Pro Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His
-40 -35 -30

AGC ACG GCC AGG ATA GTA ATG CCT CTG CAT TAC AGC CTC GTC TTC ATC 208
Ser Thr Ala Arg Ile Val Met Pro Leu His Tyr Ser Leu Val Phe Ile
-25 -20 -15 -10

ATT GGG CTC GTG GGA AAC TTA CTA GCC TTG GTC GTC ATT GTT CAA AAC 256
Ile Gly Leu Val Gly Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn
 -5 1 5

AGG AAA AAA ATC AAC TCT ACC ACC CTC TAT TCA ACA AAT TTG GTT ATT 304
Arg Lys Lys Ile Asn Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile
 10 15 20

TCT GAT ATA CTT TTT ACC ACC GCT TTG CCT ACA CGA ATA GCT ACT ATG 352
Ser Asp Ile Leu Phe Thr Thr Ala Leu Pro Thr Arg Ile Ala Thr Met
 25 30 35

CMA TGG GCY TTG ACT GGA GAA TCG GAG ATG TGG 385
Xaa Trp Ala Leu Thr Gly Glu Ser Glu Met Trp
 40 45 50

```

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Pancreas

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..462
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 99  
 region 1..408  
 id HUMORF06  
 vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..218  
id W77946  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 216..365  
id W77946  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 412..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 366..416  
id W77946  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..409  
id C16991  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 212..411  
id N28784  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 52..214  
id N28784  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..58

id N28784  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..303  
id C17735  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 303..408  
id C17735  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 47..209  
id AA057588  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 207..350  
id AA057588  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 406..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 351..407  
id AA057588  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..53  
id AA057588  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 357..443 -
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7  
seq SMIGIGSLPSCWA/CW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```

AGTTCGTTTA TTCCTCCGCG CGCTGGGACA GGCTGCTTCT TCGCCAGAAC CAACCGGTTG 60
CTTGCTGTCC CAGCGGCGCC CCCTCATCAC CGTCGCCATG CCCGGAGGTC TGCTTCTCGG 120
GGACGTGGCT CCCAACTTTG AGGCCAATAC CACCGTCGGC CGCATCCGTT TCCACGACTT 180
TCTGGGAKAC TCATGGGGCA TTCTCTTCTC CCACCCTCGG GACTTTACCC CASTGTGCAC 240
CACAGAGCTT GGCAGAGCTG CAAAGCTGGC ACCAGAATTT GCCAAGAGGA ATGTTAAGTT 300
GWTTGCCCTT TCAATAGACA GTGTTGAGGA CCATCTTGCC TGGAGCAAGG ATATCA ATG 359
 Met
CTT ACA ATT GTG AAG AGC CCA CAG AAA AGT TAC CTT TTC CCA TCA TCG 407
Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser Ser
 -25 -20 -15

ATG ATA GGA ATC GGG AGC TTG CCA TCC TGT TGG GCA TGC TGG ATC CAG 455
Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile Gln
 -10 -5 1

CAG AGA
Gln Arg
 5
 461

```

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 15  
seq LFLLLLLLAASAWG/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

```

Met Ser Ser Trp Ser Arg Gln Arg Pro Lys Ser Pro Gly Gly Ile Gln
-35 -30 -25 -20

Pro His Val Ser Arg Thr Leu Phe Leu Leu Leu Leu Ala Ala Ser
 -15 -10 -5

```

Ala Trp Gly Val Thr Leu Ser Pro Lys Asp Cys Gln Val Phe Arg Ser  
                   1                                  5                                  10  
 Asp His Gly Ser Ser Ile Ser Cys Gln Pro Pro Ala Glu Ile Pro Gly  
           15                                  20                                  25  
 Tyr Leu Pro Ala Thr  
           30

## (2) INFORMATION FOR SEQ ID NO: 293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.2  
seq LLLXAVLLSLASA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Xaa Ala Val Leu Leu  
      -20                                  -15                                  -10  
 Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser  
      -5                                  1                                  5                                  10  
 Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His  
           15                                  20                                  25  
 Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu  
           30                                  35                                  40  
 Glu Ser Glu Leu Glu Xaa Ser Ile Gln Glu Glu Glu Asp Ser Leu Lys  
           45                                  50                                  55  
 Ser Gln Glu Gly Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser  
      60                                  65                                  70                                  75

## (2) INFORMATION FOR SEQ ID NO: 294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -21..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 13.1  
seq CVLLLLLLLLLTRS/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu  
-20 -15 -10  
Leu Leu Thr Arg Ser Ser Glu Val Glu Xaa Xaa Ala Glu Val Gly Gln  
-5 1 5 10  
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu  
15 20 25  
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly  
30 35 40  
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser  
45 50 55  
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr  
60 65 70 75  
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile  
80 85 90  
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu  
95 100

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -21..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6  
seq LLFLFLAVDEAWA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Gly Pro Val Arg Leu Gly Ile Leu Leu Phe Leu Phe Leu Ala Val  
-20 -15 -10

Asp Glu Ala Trp Ala Gly Met Leu Lys Glu Glu Gly Arg  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 296: -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq SLLLAVALGLATA/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Met Lys Ser Leu Ser Leu Leu Leu Ala Val Ala Leu Gly Leu Ala Thr  
-15 -10 -5

Ala Val Ser Ala Gly Pro Ala Val Ile Glu Cys Trp Phe Val Glu Asp  
1 5 10 15

Ala Ser Gly Lys Gly Leu Ala Lys Arg Pro Gly Ala Leu Leu Leu Arg  
20 25 30

Gln Gly Pro Gly Glu Pro Pro Pro Arg Pro Asp Leu Asp Pro Glu Leu  
35 40 45

Tyr Leu Ser Val His Asp Pro Ala Gly Ala Leu Gln Ala Arg  
50 55 60

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.6  
seq LLTLXLLGGPTWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Leu Leu Leu Leu Thr Leu Xaa Leu Leu Gly Gly Pro Thr Trp Ala  
-15 -10 -5  
Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu  
1 5 10 15  
Asp Tyr Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu  
20 25 30  
Leu Val Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys  
35 40 45  
Leu Gly Ala Leu Xaa Gly Asn Thr Gln Glu Val Xaa Xaa Gln Pro Gly  
50 55 60  
Glu Tyr Ile Thr Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly  
65 70 75 80  
Met Val Met Tyr Thr Ser Lys Asp Arg  
85

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.4  
seq LIILIXIWIWCLG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:



```

Met Lys Ile Gly Ile Leu Leu Ser Leu Leu Asn Ser Val Ile Ser Gln
-45 -40 -35

Thr Leu Met Ser Cys Asn Trp Lys Gln Gln Met Arg Arg Met Lys Thr
-30 -25 -20 -15

Ile Leu Ile Ile Leu Ile Xaa Ile Trp Ile Trp Cys Leu Gly Ser Gln
 -10 -5 1

Thr Phe Gly Thr Ser Thr Thr Lys Ser Val Gln Leu Lys Ile Leu Arg
 5 10 15

Gln Asn Leu Ser His Phe Leu Gln Pro Pro Gln Val Ile
20 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.4  
seq LPFLLSLFPGALP/VQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

Met Lys Ala Ser Ser Gly Arg Cys Gly Leu Val Arg Trp Leu Gln Val
-30 -25 -20 -15

Leu Leu Pro Phe Leu Leu Ser Leu Phe Pro Gly Ala Leu Pro Val Gln
 -10 -5 1

Ile Arg Tyr Ser Ile Pro Glu Glu Leu Ala Lys Asn Ser Val Val Gly
 5 10 15

Asn Leu Ala Lys Asp Leu Gly Leu Ser Val Arg Asp Leu Pro Ala Arg
20 25 30

Lys Leu Arg Val Ser Ala Glu Lys Glu Tyr Phe Thr Val Asn Pro Glu
35 40 45 50

Ser Gly Asp Leu Leu Val Ser Asp Arg Ile Asp Arg Asp Val
 55 60

```

## (2) INFORMATION FOR SEQ ID NO: 300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1  
seq IIFLCHLLRGLHA/XT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ile Val Asp Cys Val Ser Ser His Leu Lys Lys Thr Gly Asp Gly  
-30 -25 -20

Ala Lys Thr Phe Ile Ile Phe Leu Cys His Leu Leu Arg Gly Leu His  
-15 -10 -5

Ala Xaa Thr Asp Arg Glu Lys Asp Pro Leu Met Cys Glu Asn Ile Gln  
1 5 10 15

Thr His Gly Arg Leu Pro  
20

## (2) INFORMATION FOR SEQ ID NO: 301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -104..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1  
seq LTSLSWLLXASCS/KP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Met Ala Lys Ala Leu Leu Phe Pro Ser Gly Arg Ser Val Arg Val Leu

```

-100 -95 -90
Tyr Gly Ala Val Asn Lys Glu Arg Gln Xaa Glu Ser Val Leu Asn Arg
-85 -80 -75
Ala Cys Pro Pro Lys Ala Asn Ser Lys Glu Arg Arg Gly Arg Ala Val
-70 -65 -60
Leu Gly Ala Glu Leu Thr Gln Trp Ser Ser Pro Thr Thr Ala Gly Ser
-55 -50 -45
Cys Cys Ser Ser Cys Thr Leu Cys Ala Arg Ser Ser Ser Xaa Val Ile
-40 -35 -30 -25
Ala Pro Ser Pro Leu Val Pro Phe Thr Ser Gly Leu Thr Ser Leu Ser
-20 -15 -10
Trp Leu Leu Xaa Ala Ser Cys Ser Lys Pro Xaa Lys Gly
-5 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 302:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq LATKLLSLSGVFA/VH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```

Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
-70 -65 -60
Asp Thr Ser Pro Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
-55 -50 -45
Ala Thr Pro Ser Ala Arg Ala Ala Ala Ala Val Val Ala Ala Ala Ala
-40 -35 -30
Arg Thr Gly Ser Glu Ala Arg Val Ser Lys Ala Ala Leu Ala Thr Lys
-25 -20 -15 -10
Leu Leu Ser Leu Ser Gly Val Phe Ala Val His Lys Pro Lys Gly Pro
-5 1 5
Thr Ser Ala Glu Leu Leu Asn Arg Leu Lys Glu Lys Leu Leu Ala Glu

```

10 15 20

Ala Gly Met Pro Ser Pro Glu Trp Thr Xaa Arg Lys Lys Gln Thr Xaa  
 25 30 35

Glu Asn Trp Ala Trp Arg Asp Ser Arg Gln Arg Xaa Arg Gly Val Leu  
 40 45 50 55

Val Val Gly Ile Gly Ala  
 60

## (2) INFORMATION FOR SEQ ID NO: 303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq VLWLISFFTFDTG/HG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp  
 -15 -10 -5

Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu  
 1 5 10 15

Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Met  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 304:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrenals

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq WIFLAAILKGVQC/EV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```

Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly
 -15 -10 -5

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 1 5 10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
 15 20 25

Thr Asp Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45

Glu Trp Val Ala Asn Ile Xaa Ser Thr Ala Ser Gly Gly Thr Arg Gly
 50 55 60

Tyr Ala Ala Pro Val Lys Asp Arg Phe Ile Ile Ser Arg Asp Asp Ser
 65 70 75

Arg Asn Thr Leu His Leu Gln Met Asn Gly Leu Lys Xaa Met Thr Gln
 80 85 90

Ala Ile Tyr Tyr Cys Ala Thr
 95 100

```

## (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq LWRLLLWAGTAFQ/VX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

Met Ala Glu Pro Gly His Ser His His Leu Ser Ala Arg Val Arg Gly
 -35 -30 -25

```

Arg Thr Glu Arg Arg Ile Pro Arg Leu Trp Arg Leu Leu Leu Trp Ala  
 -20 -15 -10  
 Gly Thr Ala Phe Gln Val Xaa Gln Gly Xaa Xaa Pro Glu Leu Xaa Ala  
 -5 1 5 10  
 Cys Lys Glu Ser Glu Tyr His Tyr Glu Tyr Thr Ala Cys Asp Ser Thr  
 15 20 25  
 Gly Ser Arg Trp Arg Val Ala Val Pro His Thr Xaa Gly Leu Cys Thr  
 30 35 40  
 Ser Leu Pro Asp Pro Val Lys Gly Thr Glu Cys Xaa Xaa Ser Cys Asn  
 45 50 55  
 Ala Gly Glu Phe Leu Asp Met Lys Asp Gln Ser Cys Xaa Pro Cys Ala  
 60 65 70 75  
 Glu Gly Arg Tyr Ser Leu Gly Thr Gly Ile Arg Phe Asp Glu Trp Asp  
 80 85 90  
 Glu Leu Pro His Gly Phe Ala Ala Ser Gln Pro Thr Trp Ser Trp Met  
 95 100 105  
 Thr Val Leu Leu Ser His  
 110

## (2) INFORMATION FOR SEQ ID NO: 306:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq QACLLGLFALILS/GK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

Met Thr Ala Asp Pro Arg Lys Gly Arg Met Gly Leu Gln Ala Cys Leu  
 -25 -20 -15 -10  
 Leu Gly Leu Phe Ala Leu Ile Leu Ser Gly Lys Cys Ser Xaa Ser Pro  
 -5 1 5  
 Glu Pro Asp Gln Arg Arg Thr Leu Pro Pro Gly Trp Val Ser Leu Gly  
 15 20

```

Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln
 25 30 35

Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro
 40 45 50 55

Ser Ser Pro Gln Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp
 60 65 70

Leu Val Arg Pro Ser Pro Leu Thr Pro
 75 80

```

## (2) INFORMATION FOR SEQ ID NO: 307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq LCFLLLAVAMSFF/GS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
-20 -15 -10

Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
-5 1 5

Thr Arg Ala His Leu Leu Leu Lys Xaa Lys Met Met Arg Leu Gly Gly
10 15 20

Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
25 30 35 40

Thr Leu Xaa Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
45 50 55

Pro Pro Ser Met His Phe Phe
60

```

## (2) INFORMATION FOR SEQ ID NO: 308:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.8  
seq LVLVLVVAVTVRA/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ala | Pro | Leu | Val | Leu | Val | Leu | Val | Val | Ala | Val | Thr | Val | Arg |  |
|     | -15 |     |     |     |     | -10 |     |     |     |     |     | -5  |     |     |     |  |
| Ala | Ala | Leu | Phe | Arg | Ser | Ser | Leu | Ala | Glu | Phe | Ile | Ser | Glu | Arg | Val |  |
|     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Glu | Val | Val | Ser | Pro | Leu | Ser | Ser | Trp | Lys | Arg | Val | Val | Glu | Gly | Leu |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |
| Ser | Leu | Leu | Asp | Leu | Gly | Val | Ser | Pro | Tyr | Ser | Gly | Ala | Val | Phe | His |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |  |
| Glu | Thr | Pro | Leu | Ile | Ile | Tyr | Leu | Phe | His | Phe | Leu | Ile | Asp | Tyr | Ala |  |
|     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |  |
| Glu | Leu | Val | Phe | Met | Ile | Thr | Asp | Ala | Leu | Thr | Ala | Ile | Ala | Leu | Tyr |  |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |  |
| Phe | Ala | Ile | Gln | Asp | Phe | Asn | Lys | Val | Val | Phe | Lys | Lys | Gln | Lys | Leu |  |
|     | 80  |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |  |
| Leu | Leu | Glu | Leu | Asp | Gln | Tyr | Ala | Pro | Asp | Val | Ala | Glu | Leu | Ile | Arg |  |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |  |

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide



(B) LOCATION: -102..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.7  
 seq LXMTLMPLPKILS/DS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

```

Met Thr Ala Ala Ile Arg Arg Gln Arg Glu Leu Ser Ile Leu Pro Lys
 -100 -95 -90

Val Thr Leu Glu Ala Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg
 -85 -80 -75

Ser Glu Arg Cys Pro Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro
 -70 -65 -60 -55

Ala Leu Tyr Thr Val Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu
 -50 -45 -40

Ala Leu Trp Val Phe Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile
 -35 -30 -25

Tyr Leu Lys Asn Thr Leu Val Ala Asp Leu Xaa Met Thr Leu Met Leu
 -20 -15 -10

Pro Phe Lys Ile Leu Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg
 -5 1 5 10

Ala Phe Val Cys Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr
 15 20 25

Val Gly Glu Gly
 30

```

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Spleen

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -46..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
 seq SIGVLTLSHLISG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```

Met Ser Ser Val Leu Ala Ala Ser His Pro Leu Val Leu Ser Ser Asn

```

-45

-40

-35

Ala Gly Thr Pro Gly Ile Ser Glu Lys Asp Asn Arg Asp Pro Ala Gly  
 -30 -25 -20 -15

Ser Ser Ile Gly Val Leu Thr Leu Ser His Leu Ile Ser Gly Leu Arg  
 -10 -5 1

Thr Leu Tyr Thr Leu Leu His Phe Pro Leu Arg  
 5 10

## (2) INFORMATION FOR SEQ ID NO: 311:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Thyroid

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -50..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3  
seq LIILGLVLFMVYG/NV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Met Gly Leu Ala Met Glu His Gly Gly Ser Tyr Ala Arg Ala Gly Gly  
 -50 -45 -40 -35

Ser Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr Phe Phe Leu Phe Val  
 -30 -25 -20

Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val  
 -15 -10 -5

Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu  
 1 5 10

Arg Arg Ala Glu Gly Leu Tyr Xaa Gln Leu Leu Gly Leu Thr Ala Ser  
 15 20 25 30

Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp  
 35 40 45

Ala Ile Met Gln Met Trp Leu Asn Ala  
 50 55

## (1) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 66 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -64..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 6.3  
                            seq SCLVSGWGLLANG/QR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro  
                    -60                    -55                    -50

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser  
                    -45                    -40                    -35

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr  
                    -30                    -25                    -20

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly  
                    -15                    -10                    -5

Gln Arg  
  1

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 142 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -47..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 6.3  
                            seq VICCVLFLLFILG/YI
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

```

Met Gly Gly Lys Gln Arg Asp Glu Asp Asp Glu Ala Tyr Gly Lys Pro
 -45 -40 -35
Val Lys Tyr Asp Pro Ser Phe Arg Gly Pro Ile Lys Asn Arg Ser Cys
 -30 -25 -20
Thr Asp Val Ile Cys Cys Val Leu Phe Leu Leu Phe Ile Leu Gly Tyr
 -15 -10 -5 1
Ile Val Val Gly Ile Val Ala Trp Leu Tyr Gly Asp Pro Arg Gln Val
 5 10 15
Leu Tyr Pro Arg Asn Ser Thr Gly Ala Tyr Cys Gly Met Gly Glu Asn
 20 25 30
Lys Asp Lys Pro Tyr Leu Leu Tyr Phe Asn Ile Phe Ser Cys Ile Leu
 35 40 45
Ser Ser Asn Ile Ile Ser Val Ala Glu Asn Gly Leu Gln Cys Pro Thr
 50 55 60 65
Pro Gln Val Cys Val Ser Ser Cys Pro Glu Asp Pro Trp Thr Xaa Xaa
 70 75 80
Lys Thr Ser Ser His Arg Leu Leu Gly Lys Ser Ser Ile Gln
 85 90 95

```

## (2) INFORMATION FOR SEQ ID NO: 314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq VLLFLAWVCFLFY/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```

Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe Leu
 -15 -10 -5
Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu Thr Arg
 1 5 10
Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro Gly Pro Gly
 15 20 25 30

```

Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala Cys Trp Met Ala  
                   35                                  40                                  45

Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile Asp Ala Leu Arg Phe  
                   50                                  55                                  60

Asp Phe Ala Gln Pro Gln His Ser His Val Pro Arg Glu Pro Pro Val  
                   65                                  70                                  75

Ser Leu Pro Phe Leu Gly Lys Leu Ser Ser Leu Gln Arg Ile Leu Glu  
                   80                                  85                                  90

Ile Gln Pro His His Ala Arg Leu  
                   95                                  100

## (2) INFORMATION FOR SEQ ID NO: 315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq CWMMLLGSGXSFL/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Met Ser Pro Val Leu His Phe Tyr Val Arg Pro Ser Gly His Glu Gly  
   -80                                  -75                                  -70

Ala Ala Ser Gly His Thr Arg Arg Lys Leu Gln Gly Lys Leu Pro Glu  
  -65                                  -60                                  -55                                  -50

Leu Gln Gly Val Glu Thr Glu Leu Cys Tyr Asn Val Asn Trp Thr Ala  
                   -45                                  -40                                  -35

Glu Ala Leu Pro Ser Ala Glu Glu Thr Lys Lys Leu Met Trp Leu Phe  
                   -30                                  -25                                  -20

Gly Cys Pro Tyr Cys Trp Met Met Leu Leu Gly Ser Xaa Gly Ser Phe  
                   -15                                  -10                                  -5

Leu Ala Pro Met Thr Cys Xaa Trp Arg Ser  
   1                                  5

## (2) INFORMATION FOR SEQ ID NO: 316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq ILRLLGSLSNAYS/PR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly  
-35 -30 -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser  
-20 -15 -10 -5

Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met  
1 5 10

Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp  
15 20 25

Pro Ser Asn Met Tyr Thr Lys Tyr Tyr Ile His Arg Asn Gly  
30 35 40

## (2) INFORMATION FOR SEQ ID NO: 317:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq LLRVLNLPNHSIG/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Met Gly Val Ala Lys Leu Thr Leu Leu Arg Val Leu Asn Leu Pro  
 -20 -15 -10

His Asn Ser Ile Gly Cys Val Glu Gly Leu Lys Glu Leu Val His Leu  
 -5 1 5 10

Glu Trp Leu Asn Leu Ala Gly Asn Asn Leu Lys Ala Met Glu Gln Xaa  
 15 20 25

Asn Ser Cys Thr Ala Leu Gln His Leu Asp  
 30 35

## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq ILRLLGSLSNAYS/PR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly  
 -35 -30 -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser  
 -20 -15 -10 -5

Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met  
 1 5 10

Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp  
 15 20 25

Arg

## (2) INFORMATION FOR SEQ ID NO: 319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Colon

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5  
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```
Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
 -10 -5 1
Ala Ala Ser Met Gln Glu Glu Val Arg Thr Ala Pro Arg Ala Leu
 5 10 15
```

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -47..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3  
seq GCGMFTFLSSVXA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```
Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
 -45 -40 -35
Gly Thr Ala Val Glu Thr Glu Gly Xaa Gly Ser Arg His Pro Pro Trp
 -30 -25 -20
Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Xaa Ala Ala
 -15 -10 -5 1
Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
 5 10 15
Leu Leu Gln Ile Lys Thr Leu Leu Ala Xaa Ser Cys His Glu Gln Glu
```



20

25

30

Met Val Val Ser Ser Leu Val Ile Gly .  
35 40

## (2) INFORMATION FOR SEQ ID NO: 321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LLFPVGRSWSCFA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Glu Thr Phe Leu Glu Pro Asn Asn Lys Lys Leu Leu Phe Pro Val  
-20 -15 -10  
Gly Arg Ser Trp Ser Cys Phe Ala Gln Thr Xaa Ser Leu Ala Lys Tyr  
-5 1 5  
Ile Pro Tyr Ser Leu Trp Lys Tyr Ser Val Leu Ser Gly His Ser  
10 15 20

## (2) INFORMATION FOR SEQ ID NO: 322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq FLWGLALPLFFFC/WE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```

Met Gly Phe Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys Trp
-15 -10 -5 1
Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg Arg Ala
 5 10 15
Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala Met Thr Leu
 20 25 30
Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu Ser Ala Glu Thr
 35 40 45
Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Val Pro Glu Ala Glu Thr
 50 55 60 65
Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg Glu Thr Arg Ser Phe Thr
 70 75 80
Lys Thr Xaa Pro Asn Phe Met Val Leu Xaa Xaa Xaa Val Thr
 85 90 95

```

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq WLLSDILGQGATA/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

```

Met Gln Ser Thr Ser Asn His Leu Trp Leu Leu Ser Asp Ile Leu Gly
-20 -15 -10
Gln Gly Ala Thr Ala Asn Val Phe Arg Gly Arg His Lys Lys Thr Gly
-5 1 5 10
Asp Leu Phe Ala Ile Lys Val Phe Asn Asn Ile Ser Phe Leu Arg Pro
 15 20 25
Val Asp Val Gln Met Arg Glu Phe Glu Val Leu Lys Lys Leu Asn His
 30 35 40

```

Lys Asn Ile Val Lys Leu Phe Ala Ile Glu Glu Glu Thr Gly  
45 50 55

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq ICAGSVLPPYSNC/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Val Glu Ile Cys Ala Gly Ser Val Leu Pro Pro Tyr Ser Asn Cys  
-15 -10 -5

Gln Met Pro Glu Pro Ser Ile Phe Thr Leu Ile His Phe His Thr Tyr  
1 5 10 15

Tyr Cys Leu Thr Thr Pro Gln  
20

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq LLAFGTSCSVVXY/XP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

```

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn
 -40 -35 -30
Arg Val Arg Gly Val Leu Asn Trp Xaa Ser Gly Pro Arg Gly Leu Leu
 -25 -20 -15
Ala Phe Gly Thr Ser Cys Ser Val Val Xaa Tyr Xaa Pro Leu Xaa Arg
 -10 -5 1 5
Val Val Val Thr Xaa Leu Xaa Gly His Thr Ala Arg Val Asn Cys Ile
 10 15 20
Gln Trp Ile Xaa Lys Gln Xaa Gly Met
 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq QLLLATLQEAATT/QE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

```

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
-70 -65 -60 -55
Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
 -50 -45 -40
Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
 -35 -30 -25
Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu
 -20 -15 -10
Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
 -5 1 5 10
Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly
 15 20 25
Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg
 30 35 40

```

Gln Leu Ser Pro Ser  
45

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq LLPFGMLCASSTT/KC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Arg Gln Thr Leu Pro Cys Ile Tyr Phe Trp Gly Gly Leu Leu Pro  
-25 -20 -15

Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His  
-10 -5 1 5

Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp  
10 15 20

Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg  
25 30 35

Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu  
40 45 50

Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu  
55 60 65

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -110..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq HTXGLLGFRXQG/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

```

Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
-110 -105 -100 -95
Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
 -90 -85 -80
Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu Ala Arg Tyr Val
 -75 -70 -65
Ser Leu Pro Asn Gln Asn Lys Ile Trp Thr Val Thr Val Ser Pro Glu
 -60 -55 -50
Gln Asn Asp Arg Thr Pro Leu Val Met Val His Gly Phe Gly Gly Gly
 -45 -40 -35
Val Gly Leu Trp Ile Leu Asn Met Asp Ser Leu Xaa Ala Arg Arg Thr
-30 -25 -20 -15
Leu His Thr Xaa Gly Leu Leu Gly Phe Gly Arg Xaa Gln Gly Ser Ile
 -10 -5 1
Pro Lys Gly Pro Glu Gly Leu Xaa Asp Glu Phe Val Xaa Ser Ile Xaa
 5 10 15
Thr Trp Arg Glu Thr Trp
20

```

## (2) INFORMATION FOR SEQ ID NO: 329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Large intestine

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq PLSMILLSDKIQS/SK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

```

Met Lys Val Thr Gly Ile Thr Ile Leu Phe Trp Pro Leu Ser Met Ile
 -20 -15 -10

Leu Leu Ser Asp Lys Ile Gln Ser Ser Lys Arg Glu Val Gln Cys Asn
 -5 1 5

Phe Thr Glu Lys Asn Tyr Thr Leu Ile Pro Ala Asp Ile Lys Lys Asp
 10 15 20

Val Thr Ile Leu Asp Leu Ser Tyr Asn Gln Xaa Thr Leu Asn Gly Thr
 25 30 35 40

Asp Thr

```

## (2) INFORMATION FOR SEQ ID NO: 330:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -96..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq HLSWSSSAYQAWA/QE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

```

Met Ala Ala Gly Arg Ala Gln Val Pro Ser Ser Glu Gln Ala Trp Leu
 -95 -90 -85

Glu Asp Ala Gln Val Phe Ile Gln Lys Thr Leu Cys Pro Ala Val Lys
 -80 -75 -70 -65

Glu Pro Asn Val Gln Leu Thr Pro Leu Val Ile Asp Cys Val Lys Thr
 -60 -55 -50

Val Trp Leu Ser Gln Gly Arg Asn Gln Gly Ser Thr Leu Pro Leu Ser
 -45 -40 -35

Tyr Ser Phe Val Ser Val Gln Asp Leu Lys Thr His Gln Arg Leu Pro
 -30 -25 -20

Cys Cys Ser His Leu Ser Trp Ser Ser Ser Ala Tyr Gln Ala Trp Ala
 -15 -10 -5

Gln Glu Ala Gly Pro Asn Gly Asn Pro Pro Gly
 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq STCCWCTPGGAST/ID

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Ser Thr Cys Cys Trp Cys Thr Pro Gly Gly Ala Ser Thr Ile Asp  
                  -10                  -5                  1  
Phe Leu Lys Arg Tyr Ala Ser Asn Thr Pro Ser Gly Glu Phe Gln Thr  
                  5                  10                  15  
Ala Asp Glu Asp Leu Cys Tyr Cys Leu Gly  
          20                  25

## (2) INFORMATION FOR SEQ ID NO: 332:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq VVEILPYLPCLTA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe



-35

-30

-25

Ser Asn Phe Cys Xaa Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro  
 -20 -15 -10 -5

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu  
 1 5 10

Ser Gly Asn Arg Ala  
 15

## (2) INFORMATION FOR SEQ ID NO: 333:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -107..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq IVLVLLLLGRYTEE/EQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Ala Glu Ser Glu Asp Arg Ser Leu Arg Ile Val Leu Val Gly Lys  
 -105 -100 -95

Thr Gly Ser Gly Lys Ser Ala Thr Ala Asn Thr Ile Leu Gly Glu Glu  
 -90 -85 -80

Ile Phe Asp Ser Arg Ile Ala Ala Gln Ala Val Thr Lys Asn Cys Gln  
 -75 -70 -65 -60

Lys Ala Ser Arg Glu Trp Gln Gly Arg Asp Leu Leu Val Val Asp Thr  
 -55 -50 -45

Pro Gly Leu Phe Asp Thr Lys Glu Ser Leu Xaa Thr Thr Cys Lys Glu  
 -40 -35 -30

Ile Xaa Arg Cys Ile Ile Ser Ser Cys Pro Gly Pro His Ala Ile Val  
 -25 -20 -15

Leu Val Leu Leu Leu Gly Arg Tyr Thr Glu Glu Glu Gln Lys Thr Val  
 -10 -5 1 5

Ala Leu Ile Xaa Leu  
 10

## (2) INFORMATION FOR SEQ ID NO: 334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq LLXCVGNFFGSTQ/DA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```

Met Ala Gln Lys Pro Leu Arg Leu Leu Ala Cys Gly Asp Val Glu Gly
 -45 -40 -35

Lys Phe Asp Ile Leu Phe Asn Arg Val Gln Ala Ile Gln Lys Xaa Ser
 -30 -25 -20

Gly Asn Phe Asp Leu Leu Xaa Cys Val Gly Asn Phe Phe Gly Ser Thr
 -15 -10 -5

Gln Asp Ala Glu Trp Glu Glu Tyr Lys Thr Gly Ile Lys Lys Ala Pro
 1 5 10 15

Ile Gln Thr Tyr Val Leu Gly Ala Asn Asn Gln Glu Thr Val Lys Tyr
 20 25 30

Phe Gln Asp Ala Asp Gly Cys Glu Leu Ala Glu Asn Ile Thr Tyr Leu
 35 40 45

Gly Arg Gly
 50

```

## (2) INFORMATION FOR SEQ ID NO: 335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -52..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.8  
 seq RPVLLHLHQTAHA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met  
 -50 -45 -40

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr  
 -35 -30 -25

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln  
 -20 -15 -10 -5

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr  
 1 5 10

Gln Gln Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile  
 15 20 25

Ile Ala Xaa Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Xaa His  
 30 35 40

Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile  
 45 50 55

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -52..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.8  
 seq RPVLLHLHQTAHA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Xaa Trp Lys Met  
 -50 -45 -40

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr  
 -35 -30 -25

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln  
 -20 -15 -10 -5  
 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr  
 1 5 10  
 Gln Gly

## (2) INFORMATION FOR SEQ ID NO: 337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq STLASVPPAATFG/AD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Ala Ala Thr Cys Glu Ile Ser Asn Ile Phe Ser Asn Tyr Phe Ser  
 -35 -30 -25  
 Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala  
 -20 -15 -10 -5  
 Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln  
 1 5 10  
 Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro  
 15 20 25  
 Gln Xaa Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val  
 30 35 40  
 Glu Lys Asn Lys Tyr Asp Ala Thr Gly  
 45 50

## (2) INFORMATION FOR SEQ ID NO: 338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -58..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LVSFVAVSSEGTEQ/GE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Arg Asp Cys Pro Gly Val Glu Xaa Ile Leu Asp Cys Ser Xaa Arg  
-55 -50 -45  
Gln Lys Thr Glu Gly Cys Arg Leu Gln Ala Gly Lys Glu Cys Val Asp  
-40 -35 -30  
Ser Pro Val Glu Gly Gly Gln Ser Glu Ala Pro Pro Ser Leu Val Ser  
-25 -20 -15  
Phe Ala Val Ser Ser Glu Gly Thr Glu Gln Gly Glu Asp Pro Arg Ser  
-10 -5 1 5  
Glu Lys Asp His Ser Arg Pro His Lys His Arg Ala Arg His Ala Arg  
10 15 20  
Leu Arg Arg Ser Glu Ser Leu Ser Xaa Lys Gln Val Lys Glu Ala Lys  
25 30 35  
Ser Xaa Cys Lys Ser Ile Ala Leu Leu Leu Thr Asp Ala Pro Xaa Pro  
40 45 50  
Asn Ser Lys Gly Val Leu Met Phe Lys Lys Arg  
55 60 65

## (2) INFORMATION FOR SEQ ID NO: 339:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -37..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LVFNFLILITILT/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

```

Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
 -35 -30 -25
Gln His Gln Gly Ala Val Glu Leu Leu Val Phe Asn Phe Leu Leu Ile
 -20 -15 -10
Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
 -5 1 5 10
Leu His Glu Thr Gly Gly Ala Met Val Tyr
 15 20

```

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4  
seq SLLLVQLLTPCSA/QF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

```

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val
 -25 -20 -15
Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser
 -10 -5 1
Val Leu Xaa Xaa Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala
 5 10 15
Asp Leu
20

```

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -32..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 12.6  
seq LLALLTVSTPSWC/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Val Phe Leu Pro Leu Lys Trp Ser Leu Ala Thr Met Ser Phe Leu  
-30 -25 -20

Leu Ser Ser Leu Leu Ala Leu Leu Thr Val Ser Thr Pro Ser Trp Cys  
-15 -10 -5

Gln Ser Thr Glu Ala Ser Pro Lys Arg  
1 5

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -26..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.8  
seq SLLLLLLXCVHWS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Glu Ser Ala Ala Ala Leu His Phe Ser Arg Pro Ala Ser Leu Leu  
-25 -20 -15

Leu Leu Leu Leu Xaa Cys Val His Trp Ser Gln Pro Ser Leu Leu Ser  
-10 -5 1 5

Trp

(2) INFORMATION FOR SEQ ID NO: 343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20 -15 -10 -5
Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
 1 5 10
Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
 15 20 25
Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
 30 35 40
Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
 45 50 55 60
Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
 65 70 75
Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
 80 85 90
Thr Thr Asp Lys
 95

```

## (2) INFORMATION FOR SEQ ID NO: 344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.3  
seq LVLLLVLTLCSL/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```

Met Gly Pro Trp Gly Glu Pro Glu Leu Leu Val Trp Arg Pro Glu Ala
-45 -40 -35

Val Ala Ser Glu Pro Pro Val Pro Val Gly Leu Glu Val Lys Leu Gly
-30 -25 -20 -15

Ala Leu Val Leu Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro
 -10 -5 1

Ile Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser
 5 10 15

Arg Gln Lys Ala Leu Ser Pro Lys
 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1  
seq LLLQLAVLGAALA/AA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```

Met Ala Pro Leu Leu Leu Gln Leu Ala Val Leu Gly Ala Ala Leu Ala
-15 -10 -5

Ala Ala Ala Leu Val Leu Ile Ser Ile Val Ala Phe Thr Thr Ala Thr
 1 5 10 15

Lys Met Pro Ala Leu His Arg His Glu Glu Glu Lys Phe Phe Leu Asn
 20 25 30

Ala Lys Gly Gln Lys Glu Thr Leu Pro Ser Ile Trp Asp Ser Pro Thr
 35 40 45

```

Lys Gln Leu Ser Val Val Val Pro Ser Tyr Asn Glu Glu Lys Arg Leu  
 50 55 60  
 Pro Val Met Met Asp Glu Ala Leu Ser Tyr Leu Glu Lys Arg Gln Lys  
 65 70 75 80  
 Arg Asp Pro Ala Phe Thr Tyr Glu Val Ile Val Val Asp Asp Gly Ser  
 85 90 95  
 Lys Asp Gln Thr Ser Lys  
 100

## (2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.8  
seq SALLVGFLSVIFA/LV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Xaa Leu Leu Gly Ser Ala  
 -25 -20 -15  
 Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu  
 -10 -5 1 5  
 His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn  
 10 15 20  
 Trp Xaa Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile  
 25 30 35  
 Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu  
 40 45 50  
 Leu Met Lys Ser Ile His Ala Xaa Leu Asn Ala Val Ala Ala Ile Leu  
 55 60 65  
 Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn  
 70 75 80 85  
 Ile Ala Asn Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala  
 90 95 100

## (2) INFORMATION FOR SEQ ID NO: 347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq LALSLILVLAFG/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala Phe
 -15 -10 -5

Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
 1 5 10 15

Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
 20 25 30

Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
 35 40 45

Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
 50 55 60

Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro
 65 70 75

Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr
 80 85 90 95

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
 100 105 110

Gln

```

## (2) INFORMATION FOR SEQ ID NO: 348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -15..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.4  
seq AMWLLCVALAVLA/WG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp  
-15 -10 -5 1

Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu  
5 10 15

Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala  
20 25 30

His Pro Asp Asp Glu Ala Met Trp  
35 40

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -38..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.8  
seq LVFTVSLFAWICC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr  
-35 -30 -25

Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu  
-20 -15 -10

Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr  
-5 1 5 10

Pro Pro Tyr Lys Phe Val His Val Leu Xaa Gly Val Asp Ile Tyr Pro  
                   15                                  20                                  25

Glu Asn Leu Asn Ser Lys Lys Lys  
                                   30

## (2) INFORMATION FOR SEQ ID NO: 350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq GWLVLCVLAISLA/SM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys Val Leu Ala Ile Ser  
                   -15                                  -10                                  -5

Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys  
                   1                                  5                                  10

Lys Gly Glu Ala Gly Arg Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys  
                   15                                  20                                  25                                  30

Gly Glu Gln Gly Glu Pro Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln  
                                   35                                  40                                  45

Gly Leu Lys Gly Asp Gln Gly Glu Pro Gly Pro Ser Gly Asn Pro Gly  
                   50                                  55                                  60

Lys Val Gly Tyr Pro Gly Pro Ser Gly Pro Leu Gly Ala Arg Gly Ile  
                   65                                  70                                  75

Pro Gly Ile Lys Gly Thr Lys Gly Ser Pro Gly Asn Ile Lys Asp Gln  
                   80                                  85                                  90

Pro Arg Pro Ala Phe Ser Ala Ile Arg  
                   95                                  100

## (2) INFORMATION FOR SEQ ID NO: 351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq VLLTLLLI AFIFL/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Ala | Trp | Glu | Ala | Met | Ala | Pro | His | Val | Asn | Pro | Thr | Leu | Lys |  |
|     |     |     | -60 |     |     |     |     | -55 |     |     |     |     |     | -50 |     |  |
| Asp | Lys | Ala | Leu | Ser | Pro | Gln | Gln | Xaa | Xaa | Xaa | Thr | Ser | Pro | Ala | Pro |  |
|     |     | -45 |     |     |     |     | -40 |     |     |     |     |     | -35 |     |     |  |
| Cys | Xaa | Ser | Asn | His | His | Asn | Lys | Lys | His | Leu | Ile | Leu | Ala | Phe | Cys |  |
|     | -30 |     |     |     |     | -25 |     |     |     |     | -20 |     |     |     |     |  |
| Ala | Gly | Val | Leu | Leu | Thr | Leu | Leu | Leu | Ile | Ala | Phe | Ile | Phe | Leu | Ile |  |
| -15 |     |     |     |     | -10 |     |     |     | -5  |     |     |     |     |     | 1   |  |
| Ile | Lys | Ser | Tyr | Arg | Lys | Tyr | His | Ser | Lys | Pro | Gln | Ala | Pro | Gly |     |  |
|     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LLCECLLLXAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Xaa Ala Gly  
-15 -10 -5  
Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr  
1 5 10  
Asp Ala Ala Ser Gly Thr Met Arg Lys Ser Gln Ala Lys Tyr Gly Ile  
15 20 25 30  
Ser Gly Glu Lys Asp Val Ser Pro Asp Leu Ser Cys Ala Xaa Glu Ile  
35 40 45  
Ser Glu

## (2) INFORMATION FOR SEQ ID NO: 353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq LVXSLPVHCLTFA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Met Gly His Ala Met Gly Leu Val Xaa Ser Leu Pro Val His Cys Leu  
-15 -10 -5  
Thr Phe Ala Ser Ser Ala Pro Ser Ser Pro Gln Pro Thr Arg Met Trp  
1 5 10  
Phe Xaa Ala Gln Ala His Xaa Pro Pro Leu Ile Leu Gly Pro  
15 20 25

## (2) INFORMATION FOR SEQ ID NO: 354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq CFSLVLLLSIWT/TR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr  
-15 -10 -5  
Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile  
1 5 10 15  
Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
20 25 30  
Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
35 40 45  
Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
50 55 60  
Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
65 70 75 80  
Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
85 90 95  
Val Leu Ile Trp  
100

## (2) INFORMATION FOR SEQ ID NO: 355:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -59..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq VLAQLAFLSQISQ/CI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:



```

Met Leu Leu Thr Arg Lys Gln Thr Cys Gln Leu Gly Ile Leu Leu Ser
 -55 -50 -45

Ile His Arg Gln His Ser Lys Asp Leu Gln Asp Ile Val Ala Thr Leu
 -40 -35 -30

Gly Pro Arg Ser Ala Thr His Pro His Gln Pro Ala Ile Gln Val Leu
 -25 -20 -15

Ala Gln Leu Ala Phe Leu Ser Gln Ile Ser Gln Cys Ile Ile Ser Gln
 -10 -5 1 5

Arg

```

## (2) INFORMATION FOR SEQ ID NO: 356:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq IVSLLGFVATVTL/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile
 -25 -20 -15

Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe
 -10 -5 1

Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys
 5 10 15 20

Thr Ser Arg Gln Gln Ile Pro Glu Ser Gln Gly Val Ile Ser Gly Ala
 25 30 35

Val Phe Leu Ile Ile Leu Phe Cys
 40

```

## (2) INFORMATION FOR SEQ ID NO: 357:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq PASLSLLTFKVYA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Phe Lys Val Ile Gln Arg Ser Val Gly Pro Ala Ser Leu Ser Leu  
-20 -15 -10  
Leu Thr Phe Lys Val Tyr Ala Ala Pro Lys Lys Asp Ser Pro Pro Lys  
-5 1 5  
Asn Ser Val Lys Val Asp Glu Leu Ser Leu Tyr Ser Val Pro Glu Gly  
10 15 20 25  
Gln Ser Lys Tyr Val Glu Glu Ala Arg Ser Gln Leu Glu Glu Ser Ile  
30 35 40  
Ser Gln Leu Arg His Tyr Cys Glu Pro Tyr Thr Thr Trp Cys Gln Glu  
45 50 55  
Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -136...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq LISVALVQGWALG/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```

Met Ala Lys Ser Leu Leu Lys Thr Ala Ser Leu Ser Gly Arg Thr Lys
-135 -130 -125

Leu Leu His Gln Thr Gly Leu Ser Leu Tyr Ser Thr Ser His Gly Phe
-120 -115 -110 -105

Tyr Glu Glu Glu Val Lys Lys Thr Leu Gln Gln Phe Pro Gly Gly Ser
 -100 -95 -90

Ile Asp Leu Gln Lys Glu Asp Asn Gly Ile Gly Ile Leu Thr Leu Asn
-85 -80 -75

Asn Pro Ser Arg Met Asn Ala Phe Ser Gly Val Met Met Leu Gln Leu
-70 -65 -60

Leu Glu Lys Val Ile Glu Leu Glu Asn Trp Thr Glu Gly Lys Gly Leu
-55 -50 -45

Ile Val Arg Gly Ala Lys Asn Thr Phe Ser Ser Gly Ser Asp Leu Asn
-40 -35 -30 -25

Ala Val Lys Ser Leu Gly Leu Gln Arg Leu Pro Leu Ile Ser Val Ala
-20 -15 -10

Leu Val Gln Gly Trp Ala Leu Gly Gly Gly Ala Ala
-5 1

```

## (2) INFORMATION FOR SEQ ID NO: 359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq PLLKILHAAGAQG/EM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Thr Ser Phe Ser Thr Ser Ala Gln Cys Ser Thr Ser Asp Ser Ala
-40 -35 -30

Cys Arg Ile Ser Pro Gly Gln Ile Asn Xaa Val Arg Pro Lys Leu Pro
-25 -20 -15

Leu Leu Lys Ile Leu His Ala Ala Gly Ala Gln Gly Glu Met Phe Thr

```

-10

-5

1

Val Lys Glu Val Met His Tyr Leu Gly Gln Tyr Ile Met Val Lys Gln  
 5 10 15 20

## (2) INFORMATION FOR SEQ ID NO: 360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -112..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq AFAWLGVVPLTAC/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Asp Thr Ala Glu Glu Asp Ile Cys Arg Val Cys Arg Ser Glu Gly  
 -110 -105 -100

Thr Pro Glu Lys Pro Leu Tyr His Pro Cys Val Cys Thr Gly Ser Ile  
 -95 -90 -85

Lys Xaa Val His Gln Glu Cys Leu Val Gln Trp Leu Lys His Ser Arg  
 -80 -75 -70 -65

Lys Glu Tyr Cys Glu Leu Cys Lys His Arg Phe Ala Phe Thr Pro Ile  
 -60 -55 -50

Tyr Ser Pro Asp Met Pro Ser Arg Leu Pro Ile Gln Asp Ile Phe Ala  
 -45 -40 -35

Gly Leu Val Thr Ser Ile Gly Thr Ala Ile Arg Tyr Trp Phe His Tyr  
 -30 -25 -20

Thr Leu Val Ala Phe Ala Trp Leu Gly Val Val Pro Leu Thr Ala Cys  
 -15 -10 -5

Arg Ile Tyr Lys Cys Leu Phe Thr Gly Ser Val Ser Ser Leu Leu Thr  
 1 5 10 15

Leu Pro Leu Asp Met Leu Ser Thr Glu Asn Leu Leu Ala Asp Cys Leu  
 20 25 30

Gln Gly Cys Phe Val Val Thr Cys Thr Leu Cys Ala Phe Ile  
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
                        seq MLIMLGIFNVHS/AV
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu
-10 -5 1

Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Xaa Gly Pro Gln
5 10 15

Asn Ile Tyr Asn Leu Tyr Glu His Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -112..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq AAVAVGMLXASYA/AV

(21) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Gly Gly Leu Trp Arg Pro Gly Trp Arg Cys Val Pro Phe Cys Gly
-110 -105 -100

Trp Arg Trp Ile His Pro Gly Ser Pro Thr Arg Ala Ala Glu Arg Val
 -95 -90 -85
 Glu Pro Phe Leu Arg Pro Glu Trp Ser Gly Thr Gly Gly Ala Glu Arg
 -80 -75 -70 -65
 Gly Leu Arg Trp Leu Gly Thr Trp Lys Arg Cys Ser Leu Arg Ala Arg
 -60 -55 -50
 His Pro Ala Leu Gln Pro Pro Arg Arg Pro Lys Ser Ser Asn Pro Phe
 -45 -40 -35
 Thr Arg Ala Xaa Glu Glu Glu Arg Arg Arg Xaa Asn Lys Thr Thr Leu
 -30 -25 -20
 Thr Tyr Val Ala Ala Val Ala Val Gly Met Leu Xaa Ala Ser Tyr Ala
 -15 -10 -5
 Ala Val
 1

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SDPLCVLFLNTSG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Met Ala Ala Gln Cys Val Thr Lys Val Ala Leu Asn Val Ser Cys Ala
 -35 -30 -25
 Asn Leu Leu Asp Lys Asp Ile Gly Ser Lys Ser Asp Pro Leu Cys Val
 -20 -15 -10
 Leu Phe Leu Asn Thr Ser Gly Gln Gln Trp Tyr Glu Val Glu Arg Thr
 -5 1 5
 Glu Arg Ile Lys Asn Cys Leu Asn Pro Gln Phe Ser Lys Thr Phe Ile
 10 15 20 25
 Ile Asp Tyr Tyr Phe Glu Val Val Gln Lys Leu Lys Phe Gly Val Tyr
 30 35 40

Asp Ile Xaa Asn Lys Thr Ile Glu Leu Ser Asp Asp Asp Phe Leu Gly
 45 50 55

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPTHA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Thr Gly Ser Asn Glu Phe Lys Leu Asn Gln Pro Pro Glu Asp Gly
 -70 -65 -60 -55

Ile Ser Ser Val Lys Phe Ser Pro Asn Thr Ser Gln Phe Leu Leu Val
 -50 -45 -40

Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser
 -35 -30 -25

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 -20 -15 -10

Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Xaa Xaa Lys
 -5 1 5 10

Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp
 15 20 25

Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Ser
 30 35

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq AHLWCWCGSHCCST/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Gly Lys His Leu Trp Tyr Pro Gly Gln Ala Ser Ala His Leu Cys
-25 -20 -15 -10
Trp Cys Gly Ser His Cys Cys Ser Thr Cys Val Phe Glu Asp Gln Leu
-5 1 5
Ser Asp Glu Arg Phe Gln Arg Ser Asn Ala Pro Ser Val Asn Ser Asp
10 15 20

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq MLAVSLTVXLLGA/MM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Leu Ala Val Ser Leu Thr Val Xaa Leu Leu Gly Ala Met Met Leu
-10 -5 1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
5 10 15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20 25 30 35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
40 45 50

Gly Asp Val Met Phe Thr Gly Ser Trp
 55 -60

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -76..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
 seq MLELDLLVFHLWG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Ser Ser Thr Leu Ala Lys Ile Ala Glu Ile Glu Ala Glu Met Ala
 -75 -70 -65

Arg Thr Gln Lys Asn Lys Ala Thr Ala His His Leu Gly Leu Leu Lys
 -60 -55 -50 -45

Ala Arg Leu Ala Lys Leu Arg Arg Glu Leu Ile Thr Pro Lys Gly Gly
 -40 -35 -30

Gly Gly Gly Gly Pro Gly Glu Gly Phe Asp Trp Pro Arg Gln Val Met
 -25 -20 -15

Leu Glu Leu Asp Leu Leu Val Phe His Leu Trp Gly Ser Gln His Cys
 -10 -5 1

Leu Val Thr Trp Gln Gly
 5 10

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.9
seq LVLALLLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45                -40                -35                -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
                -25                -20                -15

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val
                -10                -5                1

Ser Arg Thr Asp Ser Pro Ser Pro Leu
    5                10

```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.9
seq LLSLLFLVQGAHG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```

Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu
-25                -20                -15                -10

Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe
                -5                1                5

Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr
    10                15                20

Lys Pro Thr Pro Xaa Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu
    25                30                35

```

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -88..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6
seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu
 -85 -80 -75

Ser Leu Leu Leu Phe Ala Gly Met Gln Ile Tyr Ser Arg Gln Leu Ala
 -70 -65 -60

Ser Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu
 -55 -50 -45

Phe Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe
 -40 -35 -30 -25

Gly Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu
 -20 -15 -10

Leu Leu Ala Leu Phe Ala Ser Gly Leu Ile His Xaa Val Cys Val Thr
 -5 1 5

Thr Cys Phe Ile Phe Ser Arg Val Gly Leu Tyr Tyr Ile Asn Lys Ile
 10 15 20

Ser Ser Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6
seq VFCLLAVAPGAHS/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
 -15 -10 -5

Ala His Ser Gln Glu Gln Leu Val Gln Ser Gly Ala Glu Val Leu Lys
 1 5 10

Pro Gly Ala Ser Val Asn Ile Ser Cys Arg Ala Ser Gly Phe Thr Phe
 15 20 25

Thr Asn Tyr Tyr Val His Trp Val Arg Gln Ala Pro Gly His Gly Leu
 30 35 40 45

Glu Trp Met Gly Val Ile Asn Pro Val Ser Gly Tyr Thr Ser Tyr Ala
 50 55 60

Gln Lys Leu Gln Gly Arg Leu Thr Met Thr Thr Asp Thr Ala Ala Asn
 65 70 75

Ile Val Tyr Met Asp Leu Ser Arg Leu Lys Ser Asp Asp Thr Ala Val
 80 85 90

Tyr Phe Cys Ala Lys Val Arg Cys Leu Lys Gly Ile Cys Tyr Thr Glu
 95 100 105

Asp Ala Leu Asp Leu Trp
110 115

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -113..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6

seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Ser Pro Phe Leu Ala Arg
 -110 -105 -100

Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly
 -95 -90 -85

Thr Ser Leu Ala Leu Xaa Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly
 -80 -75 -70

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile
 -65 -60 -55 -50

Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala
 -45 -40 -35

Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys
 -30 -25 -20

Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser
 -15 -10 -5

Gly Leu Ile His Arg Val Cys Val Thr Thr Cys Phe Ile Phe Ser Met
 1 5 10 15

Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser Ser
 20 25

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4
seq LMSLLLVLPVVEA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu
 -20 -15 -10

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala

-5

1

5

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Val Pro Ala Trp
10 15 20

Gly Tyr Met His Gly
25

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq ILVVLMGLPLAQA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro
-20 -15 -10 -5

Leu Ala Gln Ala Leu Asp Cys His Val Cys Xaa Tyr Asn Gly Asp Asn
1 5 10

Cys

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11

seq LLALSLLVLWTSP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
  -15                      -10                      -5

Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
  1                      5                      10                      15

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
                20                      25                      30

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
  35                      40                      45

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
  50                      55                      60

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Xaa Arg
  65                      70                      75                      80

Ser Ser Xaa Pro Met Xaa Val Xaa Arg Glu Pro Glu Ser Glu Ser Ser
                85                      90                      95

Ile Val Asn Xaa Tyr Leu Xaa Gly Glu Arg Xaa Arg
  100                      105

```

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq RLLLLPLLLAVSG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

```

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
  -20                      -15                      -10

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
  -5                      1                      5                      10

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met

```

15 20 25
 Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
 30 35 40
 Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Xaa Thr Arg
 45 50 55
 Lys Gln Arg Ile Thr Glu Thr Gly Ser Pro Tyr Gln Glu Leu Gln Gly
 60 65 70 75
 Gln Arg Ser Asp Val Tyr Ser
 80

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10
seq LCRALCLFPRVFA/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
 -20 -15 -10
 Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
 -5 1 5
 Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Xaa Pro Glu Pro
 10 15 20
 Tyr Tyr Arg Asn Leu Asp Gly Thr Ala Ser Gly Ser Cys Xaa Ala Lys
 25 30 35 40
 Met Asn Ser Arg Glu Phe Gln Arg Thr Leu Leu Ile Ser Val Arg Arg
 45 50 55
 Gln Leu

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq LMCLSLCTAFALS/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 -15 -10 -5

Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
 1 5 10

Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Xaa Tyr Asp
 15 20 25

His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Xaa Phe Asp Gln Leu
 30 35 40 45

Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
 50 55 60

Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq LLFLSQFCILSGG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg
 -30 -25 -20 -15

Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser
 -10 -5 1

Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
 5 10 15

Ser Arg Leu Pro Ala Asp Cys Ile Asp Ser Thr Thr Asn Phe Ser Cys
 20 25 30

Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Xaa Val Lys Pro Ser Val
 35 40 45 50

Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Xaa Phe Ile Ile Asn
 55 60 65

Met Thr Cys

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
 -20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
 -5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Xaa Ile Leu Phe Arg Asn Thr Thr
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile

45 50 55
Xaa Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
60 65 70 75
Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg
80 85 90
Gly Leu Ser Gly Lys Trp
95

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq LLWLALACSPVHT/XL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5
Val His Thr Xaa Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.3
seq LFVAIFAVPLILG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

```

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
  -15                      -10                      -5

Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
  1                      5                      10                      15

Val Val Tyr Tyr Tyr Thr Val Thr Pro Ile Met Met Xaa Leu Gly Xaa
      20                      25                      30

Xaa Phe Thr Ile Asp Tyr Xaa Ile Phe Glu Ser Glu
      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq VLPVILLLLLGARP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
  -20                      -15                      -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
  -5                      1                      5                      10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
      15                      20                      25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
      30                      35                      40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile
      45                      50                      55

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
      60                      65                      70                      75

```

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu
80 85

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.2
seq LLXLALACSPVHT/TL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Arg Thr Leu Phe Asn Leu Leu Xaa Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
1 5 10

Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
15 20 25

Gly Leu Val Val Thr Asp Gly
30 35

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9

seq LLCLLHFSIVSVA/AX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Gly Ser Lys Val Ala Asp Leu Leu Tyr Trp Lys Asp Thr Arg Thr
 -40 -35 -30 -25

Ser Gly Val Val Phe Thr Gly Leu Met Val Ser Leu Leu Cys Leu Leu
 -20 -15 -10

His Phe Ser Ile Val Ser Val Ala Ala Xaa Phe Gly Xaa Xaa Xaa Xaa
 -5 1 5

Xaa Gly Xaa Gln Ser Ser Xaa Arg Val Tyr Ala Lys Cys Cys Arg Pro
 10 15 20

Cys Thr Gly Gly Met Glu
 25 30

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.9
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
 -25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
 -10 -5 1

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
 5 10 15

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
 20 25 30 35

Val Lys Pro His Met
 40

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq SAVLSGFVLGALA/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

```

Met Glu Gly Glu Ser Thr Ser Ala Val Leu Ser Gly Phe Val Leu Gly
      -15                      -10                      -5

Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu Gly Phe
      1                      5                      10

Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile Thr Asp Ser
      15                      20                      25

Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp Ile Gln Lys Tyr
      30                      35                      40                      45

Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn Ser Ser Gly Glu Val
      50                      55                      60

Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser Asn Val Lys Lys Asn Val
      65                      70                      75

Val Gly Trp Tyr Lys Phe Arg Arg His Ser Asp Gln Ile Met Thr Phe
      80                      85                      90

Arg Glu Arg Leu Leu His Lys Asn Leu Gln Glu His Phe Ser Asn Gln
      95                      100                     105

Asp Leu Val Phe Leu Leu Leu Thr Pro
      110                      115

```

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -32..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
-30 -25 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
-15 -10 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1 5 10 15
Asp Pro Glu Arg
20

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -136..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.7
seq AVALSLFLGWLGA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Ala Ala Ala Trp Xaa Ser Gly Pro Ser Ala Pro Glu Ala Val Thr
-135 -130 -125
Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
-120 -115 -110 -105
Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
-100 -95 -90

Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
 -85 -80 -75
 Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val
 -70 -65 -60
 Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn
 -55 -50 -45
 Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser
 -40 -35 -30 -25
 Cys Arg Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser
 -20 -15 -10
 Leu Phe Leu Gly Trp Leu Gly Ala Asp Arg Phe
 -5 1

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6
seq LLWLALACSPVHT/TL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 -15 -10 -5
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Thr Ser Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.6
seq ASLFLLLSLTVFS/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
-40 -35 -30
Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
-25 -20 -15
Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
-10 -5 1 5
Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
10 15 20
Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
25 30 35
Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser
40 45

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.5
seq LVLGLVLPILWA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Val Ala Pro Gly Leu Val Leu Gly Leu Val Leu Pro Leu Ile Leu
-15 -10 -5
Trp Ala Asp Arg Ser Ala Gly Ile Gly Phe Arg Phe Ala Ser Tyr Ile
1 5 10

```

Asn Asn Asp Met Val Leu Gln Lys Glu Pro Ala Gly Ala Val Ile Trp
 15                20                25                30
Gly Phe Gly Thr Pro Gly Ala Thr Val Thr Val Thr Leu Arg Gln Gly
                35                40                45
Gln Glu Thr Ile Met Lys Lys Val Thr Ser Val Lys Ala His Ser Asp
                50                55                60
Thr Trp Met Val Val Leu Asp Pro Met Lys Pro Gly Gly Xaa Phe Glu
        65                70                75
Val Met Ala Gln Gln Thr Leu Glu Lys Ile Asn Phe Thr Leu Arg Val
        80                85                90
His Asp Val Leu Phe Gly Asp Val Trp Leu Cys Ser Gly Gln Ser Asn
        95                100                105                110
Met Gln Met Thr Ala Arg Val Phe Arg Trp Arg His Val Xaa Gly Leu
        115                120                125
Leu

```

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5
seq LLTIVGLILPTRG/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
-20                -15                -10
Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
-5                1                5                10
Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
        15                20                25
Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Thr Trp Pro
        30                35                40

```

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
 45 50 55
 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr Pro Arg
 60 65 70

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq LALSSLLSLLLFA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Leu Pro Phe Leu Ala Arg
 -45 -40 -35
 Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly
 -30 -25 -20
 Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly
 -15 -10 -5 1
 Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile
 5 10 15
 Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala
 20 25 30
 Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys
 35 40 45
 Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser
 50 55 60 65
 Gly Pro

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.3
seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln
-35 -30 -25 -20

Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val Ser Arg
-15 -10 -5

Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly
1 5 10

Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly
15 20 25

Asp Pro His Ser Pro Val Ile Leu Xaa Ser Tyr Leu Pro Asp Glu Phe
30 35 40 45

Ile Glu Cys Glu Asp Arg
50

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -53..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.1
seq IYALFLLVGVCA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys
 -50 -45 -40

Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly
 -35 -30 -25

Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val
 -20 -15 -10

Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly Met Glu Glu Gln
 -5 1 5 10

Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys Gly Val Val Pro
 15 20 25

Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg Leu Cys Phe Gly
 30 35 40

Leu Ala Met Xaa Tyr Leu Leu Leu Ser Leu Leu Met Ile Lys Val Lys
 45 50 55

Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn Gly Phe
 60 65 70

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -57..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq IVRLVAFCPFASS/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Val Leu Leu His Val Leu Phe Glu His Ala Val Gly Tyr Ala Leu
 -55 -50 -45

Leu Ala Leu Lys Glu Val Glu Glu Ile Ser Leu Leu Gln Pro Gln Val
 -40 -35 -30

Glu Glu Ser Val Leu Asn Leu Gly Lys Phe His Ser Ile Val Arg Leu
 -25 -20 -15 -10

Val Ala Phe Cys Pro Phe Ala Ser Ser Gln Val Ala Leu Glu Asn Ala
 -5 1 5

```

Asn Ala Val Ser Glu Gly Val Val His Glu Asp Leu Arg Leu Leu Leu
  10                      15                      20
Glu Thr His Leu Pro Ser Lys Lys Lys Lys Val Leu Leu Gly Val Gly
  25                      30                      35
Asp Pro Lys Ile Gly Ala Ala Ile Gln Glu Glu Leu Gly Tyr Asn Cys
  40                      45                      50                      55
Gln Thr Gly Gly Val Ile Ala Glu Ile Leu Arg Xaa Val Arg Leu His
  60                      65                      70
Phe His Asn Leu Val Lys Gly Ser Asp Arg Cys Xaa Gln Leu Val Lys
  75                      80                      85
His Ser Trp Gly Trp Asp Thr Ala Ile Pro Met
  90                      95

```

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

```

Met Ser Gly Gly Arg Ala Pro Ala Val Leu Leu Gly Gly Val Ala Ser
  -45                      -40                      -35
Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro Val Ala Ser
  -30                      -25                      -20
Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser
  -15                      -10                      -5                      1
Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ile Gly
  5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq LVGFILFLTRSRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

```
Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Leu Leu Val Gly
-25                      -20                      -15

Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
-10                      -5                      1                      5

Gln Glu Pro Leu His Asn Glu Glu Pro Gly
          10                      15
```

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FLLVRKLPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

```
Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
-45                      -40                      -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
-30                      -25                      -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
```


Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Ala
 30 35 40
 Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg
 45 50 55
 Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe
 60 65 70 75
 Leu Met Thr Cys

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq LLMLLLFLSELQY/YL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp Ala Tyr Pro Lys Thr
 -45 -40 -35
 Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile
 -30 -25 -20
 Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu Ser Glu Leu Gln Tyr
 -15 -10 -5
 Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asp Lys Ser Arg
 1 5 10 15
 Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro
 20 25 30
 Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val Ala Gly Glu Gln Gln
 35 40 45
 Leu Asp Val Glu His Asn Leu Phe Lys Gln Arg Leu Asp Lys Asp Gly
 50 55 60
 Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu
 65 70 75 80

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro
85 90

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
-45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
-30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
-15 -10 -5

Leu Pro Thr Gln Arg Glu Asp Gly Asn Xaa Cys Asp Phe Asp Trp Arg
1 5 10 15

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
20 25 30

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
35 40 45

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
50 55 60

Gly Leu Leu Xaa Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
65 70 75 80

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa Tyr Phe Asn Asp Lys
85 90 95

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.4
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala
 -15 -10 -5

Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val
 1 5 10

Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met
 15 20 25

Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu
 30 35 40 45

Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Ala
 50 55 60

Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg
 65 70 75

Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile
 80 85 90

Ala Cys Lys Leu Cys
 95

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala
 -15 -10 -5
Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val
 1 5 10
Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met
 15 20 25
Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu
 30 35 40 45
Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Xaa
 50 55 60
Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg
 65 70 75
Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile
 80 85 90
Ala Cys Lys Leu Cys Glu Ala Ile Cys Pro Ala Gln Ala Ile Thr Ile
 95 100 105
Glu Ala Glu
110

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq ILPLLFGCLGVFG/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
 -20 -15 -10

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
-5              1              5              10
Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
15              20              25
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
30              35              40
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
45              50              55
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
60              65              70              75
Val Xaa Xaa Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
80              85              90
Glu Ile Cys Ser
95

```

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LLLVTWVFTPVTI/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```

Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu
-25              -20              -15
Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr
-10              -5              1
Ser Leu Asp Thr Glu Xaa Ile Asp Glu Ile Leu Asn Asn Ala Leu
5              10              15

```

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LVFCVGLLTMAKA/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val Gly Leu Leu Thr
-20 -15 -10 -5

Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro Phe Thr Tyr Asp
1 5 10

Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala Gly Ile Leu Phe
15 20 25

Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys Arg Phe Arg
30 35 40

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq ALSLLLVSGLLP/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu
-20 -15 -10

Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro

-5

1

5

Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val Leu
 10 15 20 25
 Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser Ser His Thr Leu Thr
 30 35 40
 Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr Arg Lys
 45 50 55
 Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala Glu Asp
 60 65 70
 Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro Lys Ala
 75 80 85
 Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly His Lys
 90 95 100 105
 Arg Ser Xaa Asn Lys Asn Glu Gly Gln Asp
 110 115

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq IMLLSLAAFSVIS/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Ala Val His Asp Leu Ile Phe Trp Arg Asp Val Lys Lys Thr Gly
 -35 -30 -25
 Phe Val Phe Gly Thr Thr Leu Ile Met Leu Leu Ser Leu Ala Ala Phe
 -20 -15 -10 -5
 Ser Val Ile Ser Val Val Ser Tyr Leu Ile Leu Ala Leu Leu Ser Val
 1 5 10
 Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val Ile Gln Ala Val Gln Lys
 15 20 25
 Ser Glu Glu Gly His Pro Phe Lys Ala Tyr Leu Asp Val Asp Ile Thr

30 35 40
 Leu Ser Ser Glu Ala Phe His Asn Tyr Met Asn Ala Ala Met Val His
 45 50 55 60

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLWTLLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Xaa Gly Ser Val Glu Cys Thr Xaa Gly Trp Gly His Cys Ala Pro
 -30 -25 -20
 Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
 -15 -10 -5
 Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10 15
 Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr
 20 25 30
 Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val
 35 40 45
 Val Met Val Ala Thr Asn Thr Pro Pro Gly
 50 55

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
-25 -20 -15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
-10 -5 1
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
5 10 15
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
20 25 30 35
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Xaa Gly Ala Lys Xaa
40 45 50
Glu Xaa Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
55 60 65
Phe

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLWTLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Xaa Gly His Cys Ala Pro
-30 -25 -20
Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

-15 -10 -5
 Leu Leu Gly Glu Lys Thr His Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10 15
 Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Xaa Val Gly Thr
 20 25 30
 Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val
 35 40 45
 Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp
 50 55 60
 Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro
 65 70 75 80
 Lys Asp Ser Ile Gln Phe Ser Ser
 85

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq LRLCLKLAATSASA/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ala Leu Arg Leu Leu Lys Leu Ala Ala Thr Ser Ala Ser Ala Arg
 -15 -10 -5 1
 Val Val Ala Ala Gly Ala Gln Arg Val Arg Gly Ile His Ser Ser Val
 5 10 15
 Gln Cys Lys Leu Arg Tyr Gly Met Trp His Phe Leu Leu Gly Asp Lys
 20 25 30
 Ala Ser Lys Arg Leu Thr Glu Arg Ser Arg Val Ile Thr Val Asp Gly
 35 40 45
 Asn Met
 50

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq IGHFLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Pro Ser Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65 -60 -55 -50
Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
-45 -40 -35
Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
-30 -25 -20
Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
-15 -10 -5
Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
1 5 10 15
Ser Lys Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
20 25 30
Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
35 40 45
Val Trp Lys Thr
50

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -154..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ALGILVVAGCSFA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Ala Leu Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
 -150 -145 -140

Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Xaa Asp Gly Tyr
 -135 -130 -125

Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
 -120 -115 -110

Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
 -105 -100 -95

Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
 -90 -85 -80 -75

Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
 -70 -65 -60

Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
 -55 -50 -45

Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
 -40 -35 -30

Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
 -25 -20 -15

Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys
 -10 -5 1 5

Lys Ala Thr

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -70..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq LAFSLPALPLAEL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val
-70 -65 -60 -55
Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
-50 -45 -40
Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
-35 -30 -25
Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
-20 -15 -10
Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
-5 1 5 10
Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
15 20 25
Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg
30 35 40
Xaa Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Ser
45 50 55

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq KMVHLLVLSGAWG/MQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
-20 -15 -10
Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val